SEQUENCE LISTING

<110> Silver, Gary M.
Brandt, Kevin S.
Wisnewski, Nancy

<120> NOVEL CARBOXYLESTERASE NUCLEIC ACID MOLECULES, PROTEINS AND USES THE REOF

<130> FC-1-C1-PUS

<140> 09/403,942
<141> 2000-05-02

<150> PCT/US97/20598
<151> 1997-11-10

<150> 08/747,221
<151> 1996-11-12

<160> 76

<170> PatentIn version 3.1

<210> 1
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<212> DNA
<213> Ctenocephalides felis

<220>
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<222> (92)..(400)
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<222> (219)..(219)
<223> At nucleotide 219, n = unknown
At amino acid residue 43, Xaa = Ile, Thr, Lys or Arg

<220>
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<222> (275)..(275)
<223> At nucleotide 275, n = unknown
At amino acid residue 62, Xaa = Gln, Glu or Lys

<220>
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<222> (329)..(329)
<223> At nucleotide 329, n = unknown
At amino acid residue 80, Xaa = Gln, Glu or Lys

<220>
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<222> (332)..(332)
<223> At nucleotide 332, n = unknown
At amino acid residue 81, Xaa = Tyr, His, Asn or Asp

<220>

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<222> (352)..(352)
<223> At nucleotide 352, n = unknown

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tttacatcat taataaacat aaatctaata aatcttgtgg atcaagatca agtttattag 60

tgagagtgtt ggatttgtga aatatttcaa a atg aat tct tta att gta aaa 112
Met Asn Ser Leu Ile Val Lys
1 5

att tct caa gga gct att gag ggg aag gaa atg att aat gat aat gga 160
Ile Ser Gln Gly Ala Ile Glu Gly Lys Glu Met Ile Asn Asp Asn Gly
10 15 20

aag tcg ttt aga gga ttt ttg ggt ata cct tat gct aaa ccg cct ata 208
Lys Ser Phe Arg Gly Phe Leu Gly Ile Pro Tyr Ala Lys Pro Pro Ile
25 30 35

gga aat ctt ana ttt aag cct cct caa aag cct gat gat tgg aat gat 256
Gly Asn Leu Xaa Phe Lys Pro Pro Gln Lys Pro Asp Asp Trp Asn Asp
40 45 50 55

gtt cga cca gct act gaa naa gca aat ggt tgt aga tcg aaa cat atg 304
Val Arg Pro Ala Thr Glu Xaa Ala Asn Gly Cys Arg Ser Lys His Met
60 65 70

ctg cag cat cat att att gga gac naa nat tgt cta tac cta aac gtn 352
Leu Gln His His Ile Ile Gly Asp Xaa Xaa Cys Leu Tyr Leu Asn Val
75 80 85

tat gtt cca ttg act tcc aaa ttg gag aaa cta cca gta atg ttc tgg g 401
Tyr Val Pro Leu Thr Ser Lys Leu Glu Lys Leu Pro Val Met Phe Trp
90 95 100

<210> 2
<211> 103
<212> PRT
<213> Ctenocephalides felis

<220>
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<222> (43)..(43)
<223> The 'Xaa' at location 43 stands for Lys, Arg, Thr, or Ile.

<220>
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<222> (62)..(62)
<223> The 'Xaa' at location 62 stands for Lys, Glu, Gln.

<220>
<221> misc_feature
<222> (80)..(80)
<223> The 'Xaa' at location 80 stands for Lys, Glu, Gln.

<220>
<221> misc_feature
<222> (81)..(81)
<223> The 'Xaa' at location 81 stands for Asn, Asp, His, or Tyr.

<400> 2

Met Asn Ser Leu Ile Val Lys Ile Ser Gln Gly Ala Ile Glu Gly Lys
1 5 10 15

Glu Met Ile Asn Asp Asn Gly Lys Ser Phe Arg Gly Phe Leu Gly Ile
20 25 30

Pro Tyr Ala Lys Pro Pro Ile Gly Asn Leu Xaa Phe Lys Pro Pro Gln
35 40 45

Lys Pro Asp Asp Trp Asn Asp Val Arg Pro Ala Thr Glu Xaa Ala Asn
50 55 60

Gly Cys Arg Ser Lys His Met Leu Gln His His Ile Ile Gly Asp Xaa
65 70 75 80

Xaa Cys Leu Tyr Leu Asn Val Tyr Val Pro Leu Thr Ser Lys Leu Glu
85 90 95

Lys Leu Pro Val Met Phe Trp
100

<210> 3
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<213> Ctenocephalides felis

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atagacaatn ttngtctcca ataatatgat gctgcagcat atgtttcgat ctacaaccat 120

ttgcttnttc agtagctggt cgaacatcat tccaatcatc aggcttttga ggaggcttaa 180

atntaagatt tcctataggc ggtttagcat aaggtatacc caaaaatcct ctaaacgact 240

ttccattatc attaatcatt tccttcccct caatagctcc ttgagaaatt tttacaatta 300

aagaattcat tttgaaatat ttcacaaatc caacactctc actaataaac ttgatcttga 360

tccacaagat ttattagatt tatgtttatt aatgatgtaa a 401

<210> 4
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<212> DNA
<213> Ctenocephalides felis

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<222> (2)..(364)
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Ser Arg Val Ile Phe Leu Ser Cys Ile Phe Leu Phe Ser Phe Asn Phe
1 5 10 15

ata aac tgt gat tcc ccg act gta act ttg ccc caa ggc gaa ttg gtt 97
Ile Asn Cys Asp Ser Pro Thr Val Thr Leu Pro Gln Gly Glu Leu Val
20 25 30

gga aaa gct ttg acg aac gaa aat gga aaa gag tat ttt agc tac aca 145
Gly Lys Ala Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr Thr
35 40 45

ggt gta cct tat gct aaa cct cct gtt gga gaa ctt aga ttt aag cct 193
Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys Pro
50 55 60

cca cag aaa gct gag cca tgg caa ggt gtt ttc aac gcc aca tta tac 241
Pro Gln Lys Ala Glu Pro Trp Gln Gly Val Phe Asn Ala Thr Leu Tyr
65 70 75 80

gga aat gtg tgt aaa tct tta aat ttc ttc ttg aag aaa att gaa gga 289
Gly Asn Val Cys Lys Ser Leu Asn Phe Phe Leu Lys Lys Ile Glu Gly
85 90 95

gac gaa gac tgc ttg gta gta aac gtg tac gca cca aaa aca act tct 337
Asp Glu Asp Cys Leu Val Val Asn Val Tyr Ala Pro Lys Thr Thr Ser
100 105 110

gat aaa aaa ctt cca gta ttt ttc tgg 364
Asp Lys Lys Leu Pro Val Phe Phe Trp
115 120

<210> 5
<211> 121
<212> PRT
<213> Ctenocephalides felis

<400> 5

Ser Arg Val Ile Phe Leu Ser Cys Ile Phe Leu Phe Ser Phe Asn Phe
1 5 10 15

Ile Asn Cys Asp Ser Pro Thr Val Thr Leu Pro Gln Gly Glu Leu Val
20 25 30

Gly Lys Ala Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr Thr
35 40 45

Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys Pro
50 55 60

Pro Gln Lys Ala Glu Pro Trp Gln Gly Val Phe Asn Ala Thr Leu Tyr
65 70 75 80

Gly Asn Val Cys Lys Ser Leu Asn Phe Phe Leu Lys Lys Ile Glu Gly
85 90 95

Asp Glu Asp Cys Leu Val Val Asn Val Tyr Ala Pro Lys Thr Thr Ser
100 105 110

Asp Lys Lys Leu Pro Val Phe Phe Trp
115 120

<210> 6
<211> 364
<212> DNA
<213> Ctenocephalides felis

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caagcagtct tcgtctcctt caatttttctt caagaagaaa tttaaagatt tacacacatt 120

tccgtataat gtggcgttga aaacaccttg ccatggctca gctttctgtg gaggcttaaa 180

tctaagttct ccaacaggag gtttagcata aggtacacct gtgtagctaa aatactcttt 240

tccattttcg ttcgtcaaag cttttccaac caattcgcct tggggcaaag ttacagtcgg 300

ggaatcacag tttataaaat taaaactaaa caaaaaaata caacttaaaa aaataacacg 360

agac 364

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atatggactt tagactgtga ttaatttatt ttacctgaga ttttccttta ca atg ggt 118
Met Gly
1

gat ctt caa gtg act ttg tta caa ggt tct ttg aga gga aaa gag caa 166
Asp Leu Gln Val Thr Leu Leu Gln Gly Ser Leu Arg Gly Lys Glu Gln
5 10 15

att aat gaa aag gga aat gtg ttt tat agt tat tct gga att cca tat 214
Ile Asn Glu Lys Gly Asn Val Phe Tyr Ser Tyr Ser Gly Ile Pro Tyr
20 25 30

gcc aaa cct cca gtt ggt gat cta aga ttc aag cca cct caa cct gca 262
Ala Lys Pro Pro Val Gly Asp Leu Arg Phe Lys Pro Pro Gln Pro Ala
35 40 45 50

gaa cct tgg tca ggt gtc ctt gat gct act aaa gaa ggg aat agt tgt 310
Glu Pro Trp Ser Gly Val Leu Asp Ala Thr Lys Glu Gly Asn Ser Cys
55 60 65

aga tct gta cat ttt att aaa aag att aaa gta ggg gct gaa gat tgt 358
Arg Ser Val His Phe Ile Lys Lys Ile Lys Val Gly Ala Glu Asp Cys
70 75 80

cta tac ctc aat gtc tat gta cca aaa aca tca gag aaa tcc ctt ctt 406
Leu Tyr Leu Asn Val Tyr Val Pro Lys Thr Ser Glu Lys Ser Leu Leu
85 90 95

421
cca gta atg gta tgg
Pro Val Met Val Trp
100

<210> 8
<211> 103
<212> PRT
<213> Ctenocephalides felis

<400> 8

Met Gly Asp Leu Gln Val Thr Leu Leu Gln Gly Ser Leu Arg Gly Lys
1 5 10 15

Glu Gln Ile Asn Glu Lys Gly Asn Val Phe Tyr Ser Tyr Ser Gly Ile
20 25 30

Pro Tyr Ala Lys Pro Pro Val Gly Asp Leu Arg Phe Lys Pro Pro Gln
35 40 45

Pro Ala Glu Pro Trp Ser Gly Val Leu Asp Ala Thr Lys Glu Gly Asn
50 55 60

Ser Cys Arg Ser Val His Phe Ile Lys Lys Ile Lys Val Gly Ala Glu
65 70 75 80

Asp Cys Leu Tyr Leu Asn Val Tyr Val Pro Lys Thr Ser Glu Lys Ser
85 90 95

Leu Leu Pro Val Met Val Trp
100

<210> 9
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<212> DNA
<213> Ctenocephalides felis

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tagacaatct tcagccccta ctttaatctt tttaataaaa tgtacagatc tacaactatt 120

ccctttcttta gtagcatcaa ggacacctga ccaaggttct gcaggttgag gtggcttgaa 180

tcttagatca ccaactggag gtttggcata tggaattcca gaataactat aaaacacatt 240

tccctttttca ttaatttgct cttttcctct caaagaacct tgtaacaaag tcacttgaag 300

atcacccatt gtaaaggaaa atctcaggta aaataaatta atcacagtct aaagtccata 360

ttttttggct aggttcttct aaaaaatata ctaataaaaa tatgatttga tgtaatgtaa 420

a 421

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<212> DNA
<213> Ctenocephalides felis

<220>
<221> CDS
<222> (113)..(523)
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gataaataat aacaattaag caaccaaaat gcattaaaaa acacaataaa aa atg tta 118
Met Leu
1

cct cac agt agt gca tta gtt tta ttt tta ttt ttt tta ttt ttc tta 166
Pro His Ser Ser Ala Leu Val Leu Phe Leu Phe Phe Leu Phe Phe Leu
5 10 15

ttt aca cct atc ttg tgc ata cta tgg gat aac cta gat cag cat ttg 214
Phe Thr Pro Ile Leu Cys Ile Leu Trp Asp Asn Leu Asp Gln His Leu
20 25 30

tgc aga gtt caa ttt aac agg atc acg gaa gga aaa ccg ttc cga tat 262
Cys Arg Val Gln Phe Asn Arg Ile Thr Glu Gly Lys Pro Phe Arg Tyr
35 40 45 50

aaa gat cat agg aat gat gta tat tgt tct tat ttg gga att cct tat 310

Lys Asp His Arg Asn Asp Val Tyr Cys Ser Tyr Leu Gly Ile Pro Tyr
55 60 65

gcc gaa ccg cct att gga cca tta cga ttt cag tct cca aaa cca ata 358
Ala Glu Pro Pro Ile Gly Pro Leu Arg Phe Gln Ser Pro Lys Pro Ile
70 75 80

tca aat cca aaa aca gga ttc gta cag gct cga act ttg gga gac aaa 406
Ser Asn Pro Lys Thr Gly Phe Val Gln Ala Arg Thr Leu Gly Asp Lys
85 90 95

tgt ttc cag gaa agt cta ata tat tct tat gca gga agc gaa gat tgc 454
Cys Phe Gln Glu Ser Leu Ile Tyr Ser Tyr Ala Gly Ser Glu Asp Cys
100 105 110

tta tat ctg aat ata ttc acg cca gag act gtt aat tct gcg aac aat 502
Leu Tyr Leu Asn Ile Phe Thr Pro Glu Thr Val Asn Ser Ala Asn Asn
115 120 125 130

aca aaa tat cct gta atg ttc t 524
Thr Lys Tyr Pro Val Met Phe
135

<210> 11
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<212> PRT
<213> Ctenocephalides felis

<400> 11

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Phe Leu Phe Thr Pro Ile Leu Cys Ile Leu Trp Asp Asn Leu Asp Gln
20 25 30

His Leu Cys Arg Val Gln Phe Asn Arg Ile Thr Glu Gly Lys Pro Phe
35 40 45

Arg Tyr Lys Asp His Arg Asn Asp Val Tyr Cys Ser Tyr Leu Gly Ile
50 55 60

Pro Tyr Ala Glu Pro Pro Ile Gly Pro Leu Arg Phe Gln Ser Pro Lys
65 70 75 80

Pro Ile Ser Asn Pro Lys Thr Gly Phe Val Gln Ala Arg Thr Leu Gly
85 90 95

Asp Lys Cys Phe Gln Glu Ser Leu Ile Tyr Ser Tyr Ala Gly Ser Glu
100 105 110

Asp Cys Leu Tyr Leu Asn Ile Phe Thr Pro Glu Thr Val Asn Ser Ala
115 120 125

Asn Asn Thr Lys Tyr Pro Val Met Phe

130 135

<210> 12
<211> 524
<212> DNA
<213> Ctenocephalides felis

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tcagatataa gcaatcttcg cttcctgcat aagaatatat tagactttcc tggaaacatt 120

tgtctcccaa agttcgagcc tgtacgaatc ctgtttttgg atttgatatt ggttttggag 180

actgaaatcg taatggtcca ataggcggtt cggcataagg aattcccaaa taagaacaat 240

atacatcatt cctatgatct ttatatcgga acggttttcc ttccgtgatc ctgttaaatt 300

gaactctgca caaatgctga tctaggttat cccatagtat gcacaagata ggtgtaaata 360

agaaaaataa aaaaaataaa aataaaacta atgcactact gtgaggtaac atttttttatt 420

gtgtttttta atgcattttg gttgcttaat tgttattatt tatctcgttt tgtttatgat 480

aaaatagacg ttttgaagac gacatgtcta tcgtatcaac gttc 524

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<222> (3)..(1517)
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<220>
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<222> (300)..(300)
<223> At nucleotide 300, r = a or g
At amino acid residue 100, Xaa = Asn or Asp

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Phe Ser Tyr Thr Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu
1 5 10 15

ctt aga ttt aag cct cca cag aaa gct gag cca tgg caa ggt gtt ttc 95
Leu Arg Phe Lys Pro Pro Gln Lys Ala Glu Pro Trp Gln Gly Val Phe
20 25 30

aac gcc aca tta tac gga aat gtg tgt aaa tct tta aat ttc ttc ttg 143
Asn Ala Thr Leu Tyr Gly Asn Val Cys Lys Ser Leu Asn Phe Phe Leu
35 40 45

aag aaa att gaa gga gac gaa gac tgc ttg gta gta aac gtg tac gca 191
Lys Lys Ile Glu Gly Asp Glu Asp Cys Leu Val Val Asn Val Tyr Ala
50 55 60

cca aaa aca act tct gat aaa aaa ctt cca gta ttt ttc tgg gtt cat 239

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Pro Lys Thr Thr Ser Asp Lys Lys Leu Pro Val Phe Phe Trp Val His
 65                  70                  75

ggt ggt ggt ttt gtg act gga tcc gga aat tta gaa ttc caa agc cca      287
Gly Gly Gly Phe Val Thr Gly Ser Gly Asn Leu Glu Phe Gln Ser Pro
80                  85                  90                  95

gat tat tta gta rat ttt gat gtt att ttc gta act ttc aat tac cga      335
Asp Tyr Leu Val Xaa Phe Asp Val Ile Phe Val Thr Phe Asn Tyr Arg
                100                 105                 110

ttg gga cct ctc gga ttt ctg aat ttg gag ttg gag ggt gct cca gga      383
Leu Gly Pro Leu Gly Phe Leu Asn Leu Glu Leu Glu Gly Ala Pro Gly
            115                 120                 125

aat gta gga tta ttg gat cag gtg gca gct ctg aaa tgg acc aaa gaa      431
Asn Val Gly Leu Leu Asp Gln Val Ala Ala Leu Lys Trp Thr Lys Glu
        130                 135                 140

aac att gag aaa ttt ggt gga gat cca gaa aat att aca att ggt ggt      479
Asn Ile Glu Lys Phe Gly Gly Asp Pro Glu Asn Ile Thr Ile Gly Gly
    145                 150                 155

gtt tct gct ggt gga gca agt gtt cat tat ctt ttg tta tct cat aca      527
Val Ser Ala Gly Gly Ala Ser Val His Tyr Leu Leu Leu Ser His Thr
160                 165                 170                 175

acc act gga ctt tac aaa agg gca att gct caa agt gga agt gct ttt      575
Thr Thr Gly Leu Tyr Lys Arg Ala Ile Ala Gln Ser Gly Ser Ala Phe
                180                 185                 190

aat cca tgg gcc ttc caa aga cat cca gta aag cgt agt ctt caa ctt      623
Asn Pro Trp Ala Phe Gln Arg His Pro Val Lys Arg Ser Leu Gln Leu
            195                 200                 205

gct gag ata ttg ggt cat ccc aca aac aat act caa gat gct tta gaa      671
Ala Glu Ile Leu Gly His Pro Thr Asn Asn Thr Gln Asp Ala Leu Glu
        210                 215                 220

ttc tta caa aaa gcc ccc gta gac agt ctc ctg aag aaa atg cca gct      719
Phe Leu Gln Lys Ala Pro Val Asp Ser Leu Leu Lys Lys Met Pro Ala
    225                 230                 235

gaa aca gaa ggt gaa ata ata gaa gag ttt gtc ttc gta cca tca att      767
Glu Thr Glu Gly Glu Ile Ile Glu Glu Phe Val Phe Val Pro Ser Ile
240                 245                 250                 255

gaa aaa gtt ttc cca tcc cac caa cct ttc ttg gaa gaa tca cca ttg      815
Glu Lys Val Phe Pro Ser His Gln Pro Phe Leu Glu Glu Ser Pro Leu
                260                 265                 270

gcc aga atg aaa tcc gga tcc ttt aac aaa gta cct tta tta gtt gga      863
Ala Arg Met Lys Ser Gly Ser Phe Asn Lys Val Pro Leu Leu Val Gly
            275                 280                 285

ttt aac agt gca gaa gga ctt ttg ttc aaa ttc ttc atg aaa gaa aaa      911
Phe Asn Ser Ala Glu Gly Leu Leu Phe Lys Phe Phe Met Lys Glu Lys
        290                 295                 300

cca gag atg ctg aac caa gct gaa gca gat ttt gaa aga ctc gta cca      959
Pro Glu Met Leu Asn Gln Ala Glu Ala Asp Phe Glu Arg Leu Val Pro
    305                 310                 315

gcc gaa ttt gaa tta gtc cat gga tca gag gaa tcg aaa aaa ctt gca     1007
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Ala Glu Phe Glu Leu Val His Gly Ser Glu Glu Ser Lys Lys Leu Ala
320                 325                 330                 335

gaa aaa atc agg aag ttt tac ttt gac gat aaa ccc gtt cca gaa aat      1055
Glu Lys Ile Arg Lys Phe Tyr Phe Asp Asp Lys Pro Val Pro Glu Asn
                340                 345                 350

gaa cag aaa ttt att gac ttg ata gga gat att tgg ttt act aga ggt      1103
Glu Gln Lys Phe Ile Asp Leu Ile Gly Asp Ile Trp Phe Thr Arg Gly
            355                 360                 365

gtt gac aag cat gtc aag ttg tct gtg gag aaa caa gac gaa cca gtt      1151
Val Asp Lys His Val Lys Leu Ser Val Glu Lys Gln Asp Glu Pro Val
        370                 375                 380

tat tat tat gaa tat tcc ttc tcg gaa agt cat cct gca aaa gga aca      1199
Tyr Tyr Tyr Glu Tyr Ser Phe Ser Glu Ser His Pro Ala Lys Gly Thr
    385                 390                 395

ttt ggt gat cat aat ctg act ggt gca tgc cat gga gaa gaa ctt gtg      1247
Phe Gly Asp His Asn Leu Thr Gly Ala Cys His Gly Glu Glu Leu Val
400                 405                 410                 415

aat tta ttc aaa gtc gag atg atg aag ctg gaa aaa gat aaa cct aat      1295
Asn Leu Phe Lys Val Glu Met Met Lys Leu Glu Lys Asp Lys Pro Asn
                420                 425                 430

gtt cta tta aca aaa gat aga gta ctt gcc atg tgg act aac ttc atc      1343
Val Leu Leu Thr Lys Asp Arg Val Leu Ala Met Trp Thr Asn Phe Ile
            435                 440                 445

aaa aat gga aat cct act cct gaa gta aca gaa tta ttg cca gtt aaa      1391
Lys Asn Gly Asn Pro Thr Pro Glu Val Thr Glu Leu Leu Pro Val Lys
        450                 455                 460

tgg gaa cct gcc aca aaa gac aag ttg aat tat ttg aac att gat gcc      1439
Trp Glu Pro Ala Thr Lys Asp Lys Leu Asn Tyr Leu Asn Ile Asp Ala
    465                 470                 475

acc tta act ttg gga aca aat cct gag gca aac cga gtc aaa ttt tgg      1487
Thr Leu Thr Leu Gly Thr Asn Pro Glu Ala Asn Arg Val Lys Phe Trp
480                 485                 490                 495

gaa gac gcc aca aaa tct ttg cac ggt caa taataattta tgaaaattgt        1537
Glu Asp Ala Thr Lys Ser Leu His Gly Gln
                500                 505

tttaaatact ttaggtaata tattaggtaa ataaaaatta aaaaataaca atttttatgt    1597

tttatgtatt ggcttatgtg tatcagttct aattttattt atttattctt gttttgcttg    1657

ttttgaaata tcatggtttt aattttcaaa acacaacgtc gtttgttttt agcaaaattt    1717

ccaatagata tgttatatta agtactctga agtattttta tatatacact aaaatcagta    1777

aaaatacatt aactaaaaat ataagatatt ttcaataatt ttttttaaag aaaataccaa    1837

aaataaagta aaattccaaa cggaattttt gtttaactta aaaataaaat taactcttca    1897

ataattttga taattagtat ttctgatatc attagtgaaa attatatttt gataatacgt    1957

atttatattt aaaataaaat tatgt                                         1982
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<210> 14
<211> 505
<212> PRT
<213> Ctenocephalides felis

<220>
<221> misc_feature
<222> (100)..(100)
<223> The 'Xaa' at location 100 stands for Asp, or Asn.

<400> 14

Phe Ser Tyr Thr Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu
1 5 10 15

Arg Phe Lys Pro Pro Gln Lys Ala Glu Pro Trp Gln Gly Val Phe Asn
20 25 30

Ala Thr Leu Tyr Gly Asn Val Cys Lys Ser Leu Asn Phe Phe Leu Lys
35 40 45

Lys Ile Glu Gly Asp Glu Asp Cys Leu Val Val Asn Val Tyr Ala Pro
50 55 60

Lys Thr Thr Ser Asp Lys Lys Leu Pro Val Phe Phe Trp Val His Gly
65 70 75 80

Gly Gly Phe Val Thr Gly Ser Gly Asn Leu Glu Phe Gln Ser Pro Asp
85 90 95

Tyr Leu Val Xaa Phe Asp Val Ile Phe Val Thr Phe Asn Tyr Arg Leu
100 105 110

Gly Pro Leu Gly Phe Leu Asn Leu Glu Leu Glu Gly Ala Pro Gly Asn
115 120 125

Val Gly Leu Leu Asp Gln Val Ala Ala Leu Lys Trp Thr Lys Glu Asn
130 135 140

Ile Glu Lys Phe Gly Gly Asp Pro Glu Asn Ile Thr Ile Gly Gly Val
145 150 155 160

Ser Ala Gly Gly Ala Ser Val His Tyr Leu Leu Leu Ser His Thr Thr
165 170 175

Thr Gly Leu Tyr Lys Arg Ala Ile Ala Gln Ser Gly Ser Ala Phe Asn
180 185 190

Pro Trp Ala Phe Gln Arg His Pro Val Lys Arg Ser Leu Gln Leu Ala
195 200 205

Glu Ile Leu Gly His Pro Thr Asn Asn Thr Gln Asp Ala Leu Glu Phe
210 215 220

Leu Gln Lys Ala Pro Val Asp Ser Leu Leu Lys Lys Met Pro Ala Glu
225 230 235 240

Thr Glu Gly Glu Ile Ile Glu Glu Phe Val Phe Val Pro Ser Ile Glu
245 250 255

Lys Val Phe Pro Ser His Gln Pro Phe Leu Glu Glu Ser Pro Leu Ala
260 265 270

Arg Met Lys Ser Gly Ser Phe Asn Lys Val Pro Leu Leu Val Gly Phe
275 280 285

Asn Ser Ala Glu Gly Leu Leu Phe Lys Phe Phe Met Lys Glu Lys Pro
290 295 300

Glu Met Leu Asn Gln Ala Glu Ala Asp Phe Glu Arg Leu Val Pro Ala
305 310 315 320

Glu Phe Glu Leu Val His Gly Ser Glu Glu Ser Lys Lys Leu Ala Glu
325 330 335

Lys Ile Arg Lys Phe Tyr Phe Asp Asp Lys Pro Val Pro Glu Asn Glu
340 345 350

Gln Lys Phe Ile Asp Leu Ile Gly Asp Ile Trp Phe Thr Arg Gly Val
355 360 365

Asp Lys His Val Lys Leu Ser Val Glu Lys Gln Asp Glu Pro Val Tyr
370 375 380

Tyr Tyr Glu Tyr Ser Phe Ser Glu Ser His Pro Ala Lys Gly Thr Phe
385 390 395 400

Gly Asp His Asn Leu Thr Gly Ala Cys His Gly Glu Glu Leu Val Asn
405 410 415

Leu Phe Lys Val Glu Met Met Lys Leu Glu Lys Asp Lys Pro Asn Val
420 425 430

Leu Leu Thr Lys Asp Arg Val Leu Ala Met Trp Thr Asn Phe Ile Lys
435 440 445

Asn Gly Asn Pro Thr Pro Glu Val Thr Glu Leu Leu Pro Val Lys Trp
450 455 460

Glu Pro Ala Thr Lys Asp Lys Leu Asn Tyr Leu Asn Ile Asp Ala Thr
465 470 475 480

Leu Thr Leu Gly Thr Asn Pro Glu Ala Asn Arg Val Lys Phe Trp Glu
485 490 495

Asp Ala Thr Lys Ser Leu His Gly Gln
500 505

<210> 15
<211> 1982
<212> DNA
<213> Ctenocephalides felis

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ttccgtttgg aattttactt tatttttggt attttcttta aaaaaaatta ttgaaaatat 180

cttatatttt tagttaatgt atttttactg attttagtgt atatataaaa atacttcaga 240

gtacttaata taacatatct attggaaatt ttgctaaaaa caaacgacgt tgtgttttga 300

aaattaaaac catgatattt caaaacaagc aaaacaagaa taaataaata aaattagaac 360

tgatacacat aagccaatac ataaaacata aaaattgtta ttttttaatt tttatttacc 420

taatatatta cctaaagtat ttaaaacaat tttcataaat tattattgac cgtgcaaaga 480

ttttgtggcg tcttcccaaa atttgactcg gtttgcctca ggatttgttc ccaaagttaa 540

ggtggcatca atgttcaaat aattcaactt gtcttttgtg gcaggttccc atttaactgg 600

caataattct gttacttcag gagtaggatt tccatttttg atgaagttag tccacatggc 660

aagtactcta tcttttgtta atagaacatt aggtttatct ttttccagct tcatcatctc 720

gactttgaat aaattcacaa gttcttctcc atggcatgca ccagtcagat tatgatcacc 780

aaatgttcct tttgcaggat gactttccga gaaggaatat tcataataat aaactggttc 840

gtcttgtttc tccacagaca acttgacatg cttgtcaaca cctctagtaa accaaatatc 900

tcctatcaag tcaataaatt tctgttcatt ttctggaacg ggtttatcgt caaagtaaaa 960

cttcctgatt ttttctgcaa gttttttcga ttcctctgat ccatggacta attcaaattc 1020

ggctggtacg agtctttcaa aatctgcttc agcttggttc agcatctctg gtttttcttt 1080

catgaagaat ttgaacaaaa gtccttctgc actgttaaat ccaactaata aaggtacttt 1140

gttaaaggat ccggatttca ttctggccaa tggtgattct tccaagaaag gttggtggga 1200

tgggaaaact ttttcaattg atggtacgaa gacaaactct tctattattt caccttctgt 1260

ttcagctggc attttcttca ggagactgtc tacgggggct ttttgtaaga attctaaagc 1320

atcttgagta ttgtttgtgg gatgacccaa tatctcagca agttgaagac tacgctttac 1380

tggatgtctt tggaaggccc atggattaaa agcacttcca ctttgagcaa ttgccctttt 1440

gtaaagtcca gtggttgtat gagataacaa aagataatga acacttgctc caccagcaga 1500

aacaccacca attgtaatat tttctggatc tccaccaaat ttctcaatgt tttctttggt 1560

ccatttcaga gctgccacct gatccaataa tcctacattt cctggagcac cctccaactc 1620

caaattcaga aatccgagag gtcccaatcg gtaattgaaa gttacgaaaa taacatcaaa 1680

atytactaaa taatctgggc tttggaattc taaatttccg gatccagtca caaaaccacc 1740

accatgaacc cagaaaaata ctggaagttt tttatcagaa gttgtttttg gtgcgtacac 1800

gtttactacc aagcagtctt cgtctccttc aattttcttc aagaagaaat ttaaagattt 1860

acacacattt ccgtataatg tggcgttgaa aacaccttgc catggctcag ctttctgtgg 1920

aggcttaaat ctaagttctc caacaggagg tttagcataa ggtacacctg tgtagctaaa 1980

at 1982

<210> 16
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At amino acid residue 100, Xaa = Asn or Asp

<400> 16

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Phe Ser Tyr Thr Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu
1               5                  10                  15

aga ttt aag cct cca cag aaa gct gag cca tgg caa ggt gtt ttc aac        96
Arg Phe Lys Pro Pro Gln Lys Ala Glu Pro Trp Gln Gly Val Phe Asn
            20                  25                  30

gcc aca tta tac gga aat gtg tgt aaa tct tta aat ttc ttc ttg aag       144
Ala Thr Leu Tyr Gly Asn Val Cys Lys Ser Leu Asn Phe Phe Leu Lys
        35                  40                  45

aaa att gaa gga gac gaa gac tgc ttg gta gta aac gtg tac gca cca       192
Lys Ile Glu Gly Asp Glu Asp Cys Leu Val Val Asn Val Tyr Ala Pro
    50                  55                  60

aaa aca act tct gat aaa aaa ctt cca gta ttt ttc tgg gtt cat ggt       240
Lys Thr Thr Ser Asp Lys Lys Leu Pro Val Phe Phe Trp Val His Gly
65                  70                  75                  80

ggt ggt ttt gtg act gga tcc gga aat tta gaa ttc caa agc cca gat       288
Gly Gly Phe Val Thr Gly Ser Gly Asn Leu Glu Phe Gln Ser Pro Asp
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                85                  90                  95

tat tta gta rat ttt gat gtt att ttc gta act ttc aat tac cga ttg      336
Tyr Leu Val Xaa Phe Asp Val Ile Phe Val Thr Phe Asn Tyr Arg Leu
            100                 105                 110

gga cct ctc gga ttt ctg aat ttg gag ttg gag ggt gct cca gga aat      384
Gly Pro Leu Gly Phe Leu Asn Leu Glu Leu Glu Gly Ala Pro Gly Asn
        115                 120                 125

gta gga tta ttg gat cag gtg gca gct ctg aaa tgg acc aaa gaa aac      432
Val Gly Leu Leu Asp Gln Val Ala Ala Leu Lys Trp Thr Lys Glu Asn
    130                 135                 140

att gag aaa ttt ggt gga gat cca gaa aat att aca att ggt ggt gtt      480
Ile Glu Lys Phe Gly Gly Asp Pro Glu Asn Ile Thr Ile Gly Gly Val
145                 150                 155                 160

tct gct ggt gga gca agt gtt cat tat ctt ttg tta tct cat aca acc      528
Ser Ala Gly Gly Ala Ser Val His Tyr Leu Leu Leu Ser His Thr Thr
                165                 170                 175

act gga ctt tac aaa agg gca att gct caa agt gga agt gct ttt aat      576
Thr Gly Leu Tyr Lys Arg Ala Ile Ala Gln Ser Gly Ser Ala Phe Asn
            180                 185                 190

cca tgg gcc ttc caa aga cat cca gta aag cgt agt ctt caa ctt gct      624
Pro Trp Ala Phe Gln Arg His Pro Val Lys Arg Ser Leu Gln Leu Ala
        195                 200                 205

gag ata ttg ggt cat ccc aca aac aat act caa gat gct tta gaa ttc      672
Glu Ile Leu Gly His Pro Thr Asn Asn Thr Gln Asp Ala Leu Glu Phe
    210                 215                 220

tta caa aaa gcc ccc gta gac agt ctc ctg aag aaa atg cca gct gaa      720
Leu Gln Lys Ala Pro Val Asp Ser Leu Leu Lys Lys Met Pro Ala Glu
225                 230                 235                 240

aca gaa ggt gaa ata ata gaa gag ttt gtc ttc gta cca tca att gaa      768
Thr Glu Gly Glu Ile Ile Glu Glu Phe Val Phe Val Pro Ser Ile Glu
                245                 250                 255

aaa gtt ttc cca tcc cac caa cct ttc ttg gaa gaa tca cca ttg gcc      816
Lys Val Phe Pro Ser His Gln Pro Phe Leu Glu Glu Ser Pro Leu Ala
            260                 265                 270

aga atg aaa tcc gga tcc ttt aac aaa gta cct tta tta gtt gga ttt      864
Arg Met Lys Ser Gly Ser Phe Asn Lys Val Pro Leu Leu Val Gly Phe
        275                 280                 285

aac agt gca gaa gga ctt ttg ttc aaa ttc ttc atg aaa gaa aaa cca      912
Asn Ser Ala Glu Gly Leu Leu Phe Lys Phe Phe Met Lys Glu Lys Pro
    290                 295                 300

gag atg ctg aac caa gct gaa gca gat ttt gaa aga ctc gta cca gcc      960
Glu Met Leu Asn Gln Ala Glu Ala Asp Phe Glu Arg Leu Val Pro Ala
305                 310                 315                 320

gaa ttt gaa tta gtc cat gga tca gag gaa tcg aaa aaa ctt gca gaa     1008
Glu Phe Glu Leu Val His Gly Ser Glu Glu Ser Lys Lys Leu Ala Glu
                325                 330                 335

aaa atc agg aag ttt tac ttt gac gat aaa ccc gtt cca gaa aat gaa     1056
Lys Ile Arg Lys Phe Tyr Phe Asp Asp Lys Pro Val Pro Glu Asn Glu
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          340                 345                 350

cag aaa ttt att gac ttg ata gga gat att tgg ttt act aga ggt gtt     1104
Gln Lys Phe Ile Asp Leu Ile Gly Asp Ile Trp Phe Thr Arg Gly Val
        355                 360                 365

gac aag cat gtc aag ttg tct gtg gag aaa caa gac gaa cca gtt tat     1152
Asp Lys His Val Lys Leu Ser Val Glu Lys Gln Asp Glu Pro Val Tyr
    370                 375                 380

tat tat gaa tat tcc ttc tcg gaa agt cat cct gca aaa gga aca ttt     1200
Tyr Tyr Glu Tyr Ser Phe Ser Glu Ser His Pro Ala Lys Gly Thr Phe
385                 390                 395                 400

ggt gat cat aat ctg act ggt gca tgc cat gga gaa gaa ctt gtg aat     1248
Gly Asp His Asn Leu Thr Gly Ala Cys His Gly Glu Glu Leu Val Asn
                405                 410                 415

tta ttc aaa gtc gag atg atg aag ctg gaa aaa gat aaa cct aat gtt     1296
Leu Phe Lys Val Glu Met Met Lys Leu Glu Lys Asp Lys Pro Asn Val
            420                 425                 430

cta tta aca aaa gat aga gta ctt gcc atg tgg act aac ttc atc aaa     1344
Leu Leu Thr Lys Asp Arg Val Leu Ala Met Trp Thr Asn Phe Ile Lys
        435                 440                 445

aat gga aat cct act cct gaa gta aca gaa tta ttg cca gtt aaa tgg     1392
Asn Gly Asn Pro Thr Pro Glu Val Thr Glu Leu Leu Pro Val Lys Trp
    450                 455                 460

gaa cct gcc aca aaa gac aag ttg aat tat ttg aac att gat gcc acc     1440
Glu Pro Ala Thr Lys Asp Lys Leu Asn Tyr Leu Asn Ile Asp Ala Thr
465                 470                 475                 480

tta act ttg gga aca aat cct gag gca aac cga gtc aaa ttt tgg gaa     1488
Leu Thr Leu Gly Thr Asn Pro Glu Ala Asn Arg Val Lys Phe Trp Glu
                485                 490                 495

gac gcc aca aaa tct ttg cac ggt caa                                1515
Asp Ala Thr Lys Ser Leu His Gly Gln
            500                 505
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<210> 17
<211> 1515
<212> DNA
<213> Ctenocephalides felis

<400> 17

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ttcccattta actggcaata attctgttac ttcaggagta ggatttccat ttttgatgaa    180

gttagtccac atggcaagta ctctatcttt tgttaataga acattaggtt tatcttttc     240

cagcttcatc atctcgactt tgaataaatt cacaagttct tctccatggc atgcaccagt    300

cagattatga tcaccaaatg ttccttttgc aggatgactt tccgagaagg aatattcata    360

ataataaact ggttcgtctt gtttctccac agacaacttg acatgcttgt caacacctct    420

agtaaaccaa atatctccta tcaagtcaat aaatttctgt tcattttctg gaacgggttt    480
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atcgtcaaag taaaacttcc tgatttttc tgcaagtttt ttcgattcct ctgatccatg 540

gactaattca aattcggctg gtacgagtct ttcaaaatct gcttcagctt ggttcagcat 600

ctctggtttt tctttcatga agaatttgaa caaaagtcct tctgcactgt taaatccaac 660

taataaaggt actttgttaa aggatccgga tttcattctg gccaatggtg attcttccaa 720

gaaaggttgg tgggatggga aaacttttc aattgatggt acgaagacaa actcttctat 780

tatttcacct tctgtttcag ctggcatttt cttcaggaga ctgtctacgg gggctttttg 840

taagaattct aaagcatctt gagtattgtt tgtgggatga cccaatatct cagcaagttg 900

aagactacgc tttactggat gtctttggaa ggcccatgga ttaaaagcac ttccactttg 960

agcaattgcc cttttgtaaa gtccagtggt tgtatgagat aacaaaagat aatgaacact 1020

tgctccacca gcagaaacac caccaattgt aatattttct ggatctccac caaatttctc 1080

aatgttttct ttggtccatt tcagagctgc cacctgatcc aataatccta catttcctgg 1140

agcaccctcc aactccaaat tcagaaatcc gagaggtccc aatcggtaat tgaaagttac 1200

gaaaataaca tcaaaatyta ctaaataatc tgggctttgg aattctaaat ttccggatcc 1260

agtcacaaaa ccaccaccat gaacccagaa aaatactgga agtttttat cagaagttgt 1320

ttttggtgcg tacacgttta ctaccaagca gtcttcgtct ccttcaattt tcttcaagaa 1380

gaaatttaaa gatttacaca catttccgta taatgtggcg ttgaaaacac cttgccatgg 1440

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acctgtgtag ctaaa 1515

<210> 18
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<212> DNA
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<222> (1758)..(1758)
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<222> (1768)..(1768)
<223> n = unknown

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gtt att ttt tta agt tgt att ttt ttg ttt agt ttt aat ttt ata aaa      105
Val Ile Phe Leu Ser Cys Ile Phe Leu Phe Ser Phe Asn Phe Ile Lys
    5                   10                  15

tgt gat ccc ccg act gta act ttg ccc cag ggc gaa ttg gtt gga aaa      153
Cys Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu Val Gly Lys
20                  25                  30                  35

gct ttg acg aac gaa aat gga aaa gag tat ttt agc tac aca ggt gtg      201
Ala Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr Thr Gly Val
                40                  45                  50

cct tat gct aaa cct cca gtt gga gaa ctt aga ttt aag cct cca cag      249
Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys Pro Pro Gln
            55                  60                  65

aaa gct gag cca tgg aat ggt gtt ttc aac gcc aca tca cat gga aat      297
Lys Ala Glu Pro Trp Asn Gly Val Phe Asn Ala Thr Ser His Gly Asn
        70                  75                  80

gtg tgc aaa gct ttg aat ttc ttc ttg aaa aaa att gaa gga gac gaa      345
Val Cys Lys Ala Leu Asn Phe Phe Leu Lys Lys Ile Glu Gly Asp Glu
    85                  90                  95

gac tgc ttg ttg gtg aat gtg tac gca cca aaa aca act tct gac aaa      393
Asp Cys Leu Leu Val Asn Val Tyr Ala Pro Lys Thr Thr Ser Asp Lys
100                 105                 110                 115

aaa ctt cca gta ttt ttc tgg gtt cat ggt ggc ggt ttt gtg act gga      441
Lys Leu Pro Val Phe Phe Trp Val His Gly Gly Gly Phe Val Thr Gly
                120                 125                 130

tcc gga aat tta gaa ttt caa agc cca gat tat tta gta aat tat gat      489
Ser Gly Asn Leu Glu Phe Gln Ser Pro Asp Tyr Leu Val Asn Tyr Asp
            135                 140                 145

gtt att ttt gta act ttc aat tac cga ttg gga cca ctc gga ttt ttg      537
Val Ile Phe Val Thr Phe Asn Tyr Arg Leu Gly Pro Leu Gly Phe Leu
        150                 155                 160

aat ttg gag ttg gaa ggt gct cct gga aat gta gga tta ttg gat cag      585
Asn Leu Glu Leu Glu Gly Ala Pro Gly Asn Val Gly Leu Leu Asp Gln
    165                 170                 175

gta gca gct ttg aaa tgg acc aaa gaa aat att gag aaa ttt ggt gga      633
Val Ala Ala Leu Lys Trp Thr Lys Glu Asn Ile Glu Lys Phe Gly Gly
180                 185                 190                 195

gat cca gaa aat att aca att ggt ggt gtt tct gct ggt gga gca agt      681
Asp Pro Glu Asn Ile Thr Ile Gly Gly Val Ser Ala Gly Gly Ala Ser
                200                 205                 210

gtt cat tat ctt tta ttg tca cat aca acc act gga ctt tac aaa agg      729
Val His Tyr Leu Leu Leu Ser His Thr Thr Thr Gly Leu Tyr Lys Arg
            215                 220                 225

gca att gct caa agt gga agt gct tta aat cca tgg gcc ttc caa aga      777
Ala Ile Ala Gln Ser Gly Ser Ala Leu Asn Pro Trp Ala Phe Gln Arg
        230                 235                 240

cat cca gta aag cgt agt ctt caa ctt gct gag ata tta ggt cat ccc      825
His Pro Val Lys Arg Ser Leu Gln Leu Ala Glu Ile Leu Gly His Pro
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245                 250                 255

aca aac aac act caa gat gct tta gaa ttc tta caa aaa gcc cca gta      873
Thr Asn Asn Thr Gln Asp Ala Leu Glu Phe Leu Gln Lys Ala Pro Val
260                 265                 270                 275

gac agt ctc ctg aaa aaa atg cca gct gaa aca gaa ggt gaa ata ata      921
Asp Ser Leu Leu Lys Lys Met Pro Ala Glu Thr Glu Gly Glu Ile Ile
                280                 285                 290

gaa gag ttc gtc ttc gta cca tca att gaa aaa gtt ttc cca tcc cac      969
Glu Glu Phe Val Phe Val Pro Ser Ile Glu Lys Val Phe Pro Ser His
            295                 300                 305

caa cct ttc ttg gaa gaa tca cca ttg gcc aga atg aaa tct gga tcc     1017
Gln Pro Phe Leu Glu Glu Ser Pro Leu Ala Arg Met Lys Ser Gly Ser
        310                 315                 320

ttt aac aaa gta cct tta tta gtt gga ttc aac agc gca gaa gga ctt     1065
Phe Asn Lys Val Pro Leu Leu Val Gly Phe Asn Ser Ala Glu Gly Leu
    325                 330                 335

ttg tac aaa ttc ttt atg aaa gaa aaa cca gag atg ctg aac caa gct     1113
Leu Tyr Lys Phe Phe Met Lys Glu Lys Pro Glu Met Leu Asn Gln Ala
340                 345                 350                 355

gaa gca gat ttc gaa aga ctc gta cca gcc gaa ttt gaa tta gcc cat     1161
Glu Ala Asp Phe Glu Arg Leu Val Pro Ala Glu Phe Glu Leu Ala His
                360                 365                 370

gga tca gaa gaa tcg aaa aaa ctt gca gaa aaa atc agg aag ttt tac     1209
Gly Ser Glu Glu Ser Lys Lys Leu Ala Glu Lys Ile Arg Lys Phe Tyr
            375                 380                 385

ttt gac gat aaa ccc gtt cct gaa aat gag cag aaa ttt att gac ttg     1257
Phe Asp Asp Lys Pro Val Pro Glu Asn Glu Gln Lys Phe Ile Asp Leu
        390                 395                 400

ata gga gat att tgg ttt act aga ggc att gac aag cat gtc aag ttg     1305
Ile Gly Asp Ile Trp Phe Thr Arg Gly Ile Asp Lys His Val Lys Leu
    405                 410                 415

tct gta gaa aaa caa gac gag cca gta tat tat tat gaa tat tct ttc     1353
Ser Val Glu Lys Gln Asp Glu Pro Val Tyr Tyr Tyr Glu Tyr Ser Phe
420                 425                 430                 435

tct gaa agt cat cct gca aaa gga aca ttt ggt gac cat aac ttg act     1401
Ser Glu Ser His Pro Ala Lys Gly Thr Phe Gly Asp His Asn Leu Thr
                440                 445                 450

gga gca tgt cat ggt gaa gaa ctt gtg aat tta ttc aaa gtc gag atg     1449
Gly Ala Cys His Gly Glu Glu Leu Val Asn Leu Phe Lys Val Glu Met
            455                 460                 465

atg aag ctg gaa aaa gat aaa ccg aat gtt tta tta aca aaa gat agg     1497
Met Lys Leu Glu Lys Asp Lys Pro Asn Val Leu Leu Thr Lys Asp Arg
        470                 475                 480

gta ctt gct atg tgg acg aac ttc atc aaa aat gga aat cct act cct     1545
Val Leu Ala Met Trp Thr Asn Phe Ile Lys Asn Gly Asn Pro Thr Pro
    485                 490                 495

gaa gta act gaa tta ttg cca gtt aaa tgg gaa cct gcc aca aaa gac     1593
Glu Val Thr Glu Leu Leu Pro Val Lys Trp Glu Pro Ala Thr Lys Asp
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500 505 510 515

aag ttg aat tat ttg aac att gat gcc acc tta act ttg gga aca aat 1641
Lys Leu Asn Tyr Leu Asn Ile Asp Ala Thr Leu Thr Leu Gly Thr Asn
520 525 530

cca gaa gaa acc cga gtc aaa tty tgg gaa gat gcc aca aaa act ttg 1689
Pro Glu Glu Thr Arg Val Lys Phe Trp Glu Asp Ala Thr Lys Thr Leu
535 540 545

cac agt caa taa aaatgtatga aaattgtttt aattatttta ggtaatacat 1741
His Ser Gln
550

taggtaaata aaaattnaaa aataacnaaa aaaaaaaaaa aaaaaaaaaa a 1792

<210> 19
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<212> PRT
<213> Ctenocephalides felis

<400> 19

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Phe Ile Lys Cys Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu
20 25 30

Val Gly Lys Ala Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr
35 40 45

Thr Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys
50 55 60

Pro Pro Gln Lys Ala Glu Pro Trp Asn Gly Val Phe Asn Ala Thr Ser
65 70 75 80

His Gly Asn Val Cys Lys Ala Leu Asn Phe Phe Leu Lys Lys Ile Glu
85 90 95

Gly Asp Glu Asp Cys Leu Leu Val Asn Val Tyr Ala Pro Lys Thr Thr
100 105 110

Ser Asp Lys Lys Leu Pro Val Phe Phe Trp Val His Gly Gly Gly Phe
115 120 125

Val Thr Gly Ser Gly Asn Leu Glu Phe Gln Ser Pro Asp Tyr Leu Val
130 135 140

Asn Tyr Asp Val Ile Phe Val Thr Phe Asn Tyr Arg Leu Gly Pro Leu
145 150 155 160

Gly Phe Leu Asn Leu Glu Leu Glu Gly Ala Pro Gly Asn Val Gly Leu
165 170 175

Leu Asp Gln Val Ala Ala Leu Lys Trp Thr Lys Glu Asn Ile Glu Lys
180 185 190

Phe Gly Gly Asp Pro Glu Asn Ile Thr Ile Gly Gly Val Ser Ala Gly
195 200 205

Gly Ala Ser Val His Tyr Leu Leu Leu Ser His Thr Thr Thr Gly Leu
210 215 220

Tyr Lys Arg Ala Ile Ala Gln Ser Gly Ser Ala Leu Asn Pro Trp Ala
225 230 235 240

Phe Gln Arg His Pro Val Lys Arg Ser Leu Gln Leu Ala Glu Ile Leu
245 250 255

Gly His Pro Thr Asn Asn Thr Gln Asp Ala Leu Glu Phe Leu Gln Lys
260 265 270

Ala Pro Val Asp Ser Leu Leu Lys Lys Met Pro Ala Glu Thr Glu Gly
275 280 285

Glu Ile Ile Glu Glu Phe Val Phe Val Pro Ser Ile Glu Lys Val Phe
290 295 300

Pro Ser His Gln Pro Phe Leu Glu Glu Ser Pro Leu Ala Arg Met Lys
305 310 315 320

Ser Gly Ser Phe Asn Lys Val Pro Leu Leu Val Gly Phe Asn Ser Ala
325 330 335

Glu Gly Leu Leu Tyr Lys Phe Phe Met Lys Glu Lys Pro Glu Met Leu
340 345 350

Asn Gln Ala Glu Ala Asp Phe Glu Arg Leu Val Pro Ala Glu Phe Glu
355 360 365

Leu Ala His Gly Ser Glu Glu Ser Lys Lys Leu Ala Glu Lys Ile Arg
370 375 380

Lys Phe Tyr Phe Asp Asp Lys Pro Val Pro Glu Asn Glu Gln Lys Phe
385 390 395 400

Ile Asp Leu Ile Gly Asp Ile Trp Phe Thr Arg Gly Ile Asp Lys His
405 410 415

Val Lys Leu Ser Val Glu Lys Gln Asp Glu Pro Val Tyr Tyr Tyr Glu
420 425 430

Tyr Ser Phe Ser Glu Ser His Pro Ala Lys Gly Thr Phe Gly Asp His
435 440 445

Asn Leu Thr Gly Ala Cys His Gly Glu Glu Leu Val Asn Leu Phe Lys
450 455 460

Val Glu Met Met Lys Leu Glu Lys Asp Lys Pro Asn Val Leu Leu Thr
465 470 475 480

Lys Asp Arg Val Leu Ala Met Trp Thr Asn Phe Ile Lys Asn Gly Asn
485 490 495

Pro Thr Pro Glu Val Thr Glu Leu Leu Pro Val Lys Trp Glu Pro Ala
500 505 510

Thr Lys Asp Lys Leu Asn Tyr Leu Asn Ile Asp Ala Thr Leu Thr Leu
515 520 525

Gly Thr Asn Pro Glu Glu Thr Arg Val Lys Phe Trp Glu Asp Ala Thr
530 535 540

Lys Thr Leu His Ser Gln
545 550

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<213> Ctenocephalides felis

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cttcccaraa tttgactcgg gtttcttctg gatttgttcc caaagttaag gtggcatcaa 180

tgttcaaata attcaacttg tcttttgtgg caggttccca tttaactggc aataattcag 240

ttacttcagg agtaggattt ccatttttga tgaagttcgt ccacatagca agtaccctat 300

cttttgttaa taaaacattc ggtttatctt tttccagctt catcatctcg actttgaata 360

aattcacaag ttcttcacca tgacatgctc cagtcaagtt atggtcacca aatgttcctt 420

ttgcaggatg actttcagag aaagaatatt cataataata tactggctcg tcttgttttt 480

ctacagacaa cttgacatgc ttgtcaatgc ctctagtaaa ccaaatatct cctatcaagt 540

caataaattt ctgctcattt tcaggaacgg gtttatcgtc aaagtaaaac ttcctgattt 600

tttctgcaag ttttttcgat tcttctgatc catgggctaa ttcaaattcg gctggtacga 660

gtctttcgaa atctgcttca gcttggttca gcatctctgg tttttctttc ataaagaatt 720

tgtacaaaag tccttctgcg ctgttgaatc caactaataa aggtactttg ttaaaggatc 780

cagatttcat tctggccaat ggtgattctt ccaagaaagg ttggtgggat gggaaaactt 840

tttcaattga tggtacgaag acgaactctt ctattatttc accttctgtt tcagctggca 900

ttttttttcag gagactgtct actggggctt tttgtaagaa ttctaaagca tcttgagtgt 960

tgtttgtggg atgacctaat atctcagcaa gttgaagact acgctttact ggatgtcttt 1020

ggaaggccca tggatttaaa gcacttccac tttgagcaat tgccctttg taaagtccag 1080

tggttgtatg tgacaataaa agataatgaa cacttgctcc accagcagaa acaccaccaa 1140

ttgtaatatt ttctggatct ccaccaaatt tctcaatatt ttctttggtc catttcaaag 1200

ctgctacctg atccaataat cctacatttc caggagcacc ttccaactcc aaattcaaaa 1260

atccgagtgg tcccaatcgg taattgaaag ttacaaaaat aacatcataa tttactaaat 1320

aatctgggct ttgaaattct aaatttccgg atccagtcac aaaaccgcca ccatgaaccc 1380

agaaaaatac tggaagtttt ttgtcagaag ttgtttttgg tgcgtacaca ttcaccaaca 1440

agcagtcttc gtctccttca atttttttca agaagaaatt caaagctttg cacacatttc 1500

catgtgatgt ggcgttgaaa acaccattcc atggctcagc tttctgtgga ggcttaaatc 1560

taagttctcc aactggaggt ttagcataag gcacacctgt gtagctaaaa tactcttttc 1620

cattttcgtt cgtcaaagct tttccaacca attcgccctg gggcaaagtt acagtcgggg 1680

gatcacattt tataaaatta aaactaaaca aaaaaataca acttaaaaaa ataacacgag 1740

acatcttgga tctagactat tgactgtgtg tactgaatta ttagcacaca gt 1792

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<212> DNA
<213> Ctenocephalides felis

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1               5                  10                  15

ttt ata aaa tgt gat ccc ccg act gta act ttg ccc cag ggc gaa ttg      96
Phe Ile Lys Cys Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu
            20                  25                  30

gtt gga aaa gct ttg acg aac gaa aat gga aaa gag tat ttt agc tac     144
Val Gly Lys Ala Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr
        35                  40                  45

aca ggt gtg cct tat gct aaa cct cca gtt gga gaa ctt aga ttt aag     192
Thr Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys
    50                  55                  60

cct cca cag aaa gct gag cca tgg aat ggt gtt ttc aac gcc aca tca     240
Pro Pro Gln Lys Ala Glu Pro Trp Asn Gly Val Phe Asn Ala Thr Ser
65                  70                  75                  80

cat gga aat gtg tgc aaa gct ttg aat ttc ttc ttg aaa aaa att gaa     288
His Gly Asn Val Cys Lys Ala Leu Asn Phe Phe Leu Lys Lys Ile Glu
                85                  90                  95

gga gac gaa gac tgc ttg ttg gtg aat gtg tac gca cca aaa aca act     336
Gly Asp Glu Asp Cys Leu Leu Val Asn Val Tyr Ala Pro Lys Thr Thr
            100                 105                 110

tct gac aaa aaa ctt cca gta ttt ttc tgg gtt cat ggt ggc ggt ttt     384
Ser Asp Lys Lys Leu Pro Val Phe Phe Trp Val His Gly Gly Gly Phe
        115                 120                 125

gtg act gga tcc gga aat tta gaa ttt caa agc cca gat tat tta gta     432
Val Thr Gly Ser Gly Asn Leu Glu Phe Gln Ser Pro Asp Tyr Leu Val
    130                 135                 140

aat tat gat gtt att ttt gta act ttc aat tac cga ttg gga cca ctc     480
Asn Tyr Asp Val Ile Phe Val Thr Phe Asn Tyr Arg Leu Gly Pro Leu
145                 150                 155                 160

gga ttt ttg aat ttg gag ttg gaa ggt gct cct gga aat gta gga tta     528
Gly Phe Leu Asn Leu Glu Leu Glu Gly Ala Pro Gly Asn Val Gly Leu
                165                 170                 175

ttg gat cag gta gca gct ttg aaa tgg acc aaa gaa aat att gag aaa     576
Leu Asp Gln Val Ala Ala Leu Lys Trp Thr Lys Glu Asn Ile Glu Lys
            180                 185                 190

ttt ggt gga gat cca gaa aat att aca att ggt ggt gtt tct gct ggt     624
Phe Gly Gly Asp Pro Glu Asn Ile Thr Ile Gly Gly Val Ser Ala Gly
        195                 200                 205

gga gca agt gtt cat tat ctt tta ttg tca cat aca acc act gga ctt     672
Gly Ala Ser Val His Tyr Leu Leu Leu Ser His Thr Thr Thr Gly Leu
    210                 215                 220

tac aaa agg gca att gct caa agt gga agt gct tta aat cca tgg gcc     720
Tyr Lys Arg Ala Ile Ala Gln Ser Gly Ser Ala Leu Asn Pro Trp Ala
225                 230                 235                 240

ttc caa aga cat cca gta aag cgt agt ctt caa ctt gct gag ata tta     768
Phe Gln Arg His Pro Val Lys Arg Ser Leu Gln Leu Ala Glu Ile Leu
                245                 250                 255

ggt cat ccc aca aac aac act caa gat gct tta gaa ttc tta caa aaa     816
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Gly His Pro Thr Asn Asn Thr Gln Asp Ala Leu Glu Phe Leu Gln Lys
           260                 265                 270

gcc cca gta gac agt ctc ctg aaa aaa atg cca gct gaa aca gaa ggt      864
Ala Pro Val Asp Ser Leu Leu Lys Lys Met Pro Ala Glu Thr Glu Gly
       275                 280                 285

gaa ata ata gaa gag ttc gtc ttc gta cca tca att gaa aaa gtt ttc      912
Glu Ile Ile Glu Glu Phe Val Phe Val Pro Ser Ile Glu Lys Val Phe
   290                 295                 300

cca tcc cac caa cct ttc ttg gaa gaa tca cca ttg gcc aga atg aaa      960
Pro Ser His Gln Pro Phe Leu Glu Glu Ser Pro Leu Ala Arg Met Lys
305                 310                 315                 320

tct gga tcc ttt aac aaa gta cct tta tta gtt gga ttc aac agc gca     1008
Ser Gly Ser Phe Asn Lys Val Pro Leu Leu Val Gly Phe Asn Ser Ala
                325                 330                 335

gaa gga ctt ttg tac aaa ttc ttt atg aaa gaa aaa cca gag atg ctg     1056
Glu Gly Leu Leu Tyr Lys Phe Phe Met Lys Glu Lys Pro Glu Met Leu
           340                 345                 350

aac caa gct gaa gca gat ttc gaa aga ctc gta cca gcc gaa ttt gaa     1104
Asn Gln Ala Glu Ala Asp Phe Glu Arg Leu Val Pro Ala Glu Phe Glu
       355                 360                 365

tta gcc cat gga tca gaa gaa tcg aaa aaa ctt gca gaa aaa atc agg     1152
Leu Ala His Gly Ser Glu Glu Ser Lys Lys Leu Ala Glu Lys Ile Arg
   370                 375                 380

aag ttt tac ttt gac gat aaa ccc gtt cct gaa aat gag cag aaa ttt     1200
Lys Phe Tyr Phe Asp Asp Lys Pro Val Pro Glu Asn Glu Gln Lys Phe
385                 390                 395                 400

att gac ttg ata gga gat att tgg ttt act aga ggc att gac aag cat     1248
Ile Asp Leu Ile Gly Asp Ile Trp Phe Thr Arg Gly Ile Asp Lys His
                405                 410                 415

gtc aag ttg tct gta gaa aaa caa gac gag cca gta tat tat tat gaa     1296
Val Lys Leu Ser Val Glu Lys Gln Asp Glu Pro Val Tyr Tyr Tyr Glu
           420                 425                 430

tat tct ttc tct gaa agt cat cct gca aaa gga aca ttt ggt gac cat     1344
Tyr Ser Phe Ser Glu Ser His Pro Ala Lys Gly Thr Phe Gly Asp His
       435                 440                 445

aac ttg act gga gca tgt cat ggt gaa gaa ctt gtg aat tta ttc aaa     1392
Asn Leu Thr Gly Ala Cys His Gly Glu Glu Leu Val Asn Leu Phe Lys
   450                 455                 460

gtc gag atg atg aag ctg gaa aaa gat aaa ccg aat gtt tta tta aca     1440
Val Glu Met Met Lys Leu Glu Lys Asp Lys Pro Asn Val Leu Leu Thr
465                 470                 475                 480

aaa gat agg gta ctt gct atg tgg acg aac ttc atc aaa aat gga aat     1488
Lys Asp Arg Val Leu Ala Met Trp Thr Asn Phe Ile Lys Asn Gly Asn
                485                 490                 495

cct act cct gaa gta act gaa tta ttg cca gtt aaa tgg gaa cct gcc     1536
Pro Thr Pro Glu Val Thr Glu Leu Leu Pro Val Lys Trp Glu Pro Ala
           500                 505                 510

aca aaa gac aag ttg aat tat ttg aac att gat gcc acc tta act ttg     1584
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Thr Lys Asp Lys Leu Asn Tyr Leu Asn Ile Asp Ala Thr Leu Thr Leu
        515                 520                 525

gga aca aat cca gaa gaa acc cga gtc aaa tty tgg gaa gat gcc aca      1632
Gly Thr Asn Pro Glu Glu Thr Arg Val Lys Phe Trp Glu Asp Ala Thr
    530                 535                 540

aaa act ttg cac agt caa                                             1650
Lys Thr Leu His Ser Gln
545                 550
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<210> 22
<211> 1650
<212> DNA
<213> Ctenocephalides felis

<400> 22

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tgttcccaaa gttaaggtgg catcaatgtt caaataattc aacttgtctt ttgtggcagg    120

ttcccattta actggcaata attcagttac ttcaggagta ggatttccat ttttgatgaa    180

gttcgtccac atagcaagta ccctatcttt tgttaataaa acattcggtt tatcttttttc    240

cagcttcatc atctcgactt tgaataaatt cacaagttct tcaccatgac atgctccagt    300

caagttatgg tcaccaaatg ttccttttgc aggatgactt tcagagaaag aatattcata    360

ataatatact ggctcgtctt gtttttctac agacaacttg acatgcttgt caatgcctct    420

agtaaaccaa atatctccta tcaagtcaat aaatttctgc tcattttcag gaacgggttt    480

atcgtcaaag taaaacttcc tgatttttttc tgcaagtttt ttcgattctt ctgatccatg    540

ggctaattca aattcggctg gtacgagtct ttcgaaatct gcttcagctt ggttcagcat    600

ctctggtttt tctttcataa agaatttgta caaaagtcct tctgcgctgt tgaatccaac    660

taataaaggt actttgttaa aggatccaga tttcattctg gccaatggtg attcttccaa    720

gaaaggttgg tgggatggga aaacttttttc aattgatggt acgaagacga actcttctat    780

tatttcacct tctgtttcag ctggcatttt tttcaggaga ctgtctactg gggctttttg    840

taagaattct aaagcatctt gagtgttgtt tgtgggatga cctaatatct cagcaagttg    900

aagactacgc tttactggat gtctttggaa ggcccatgga tttaaagcac ttccactttg    960

agcaattgcc cttttgtaaa gtccagtggt tgtatgtgac aataaaagat aatgaacact   1020

tgctccacca gcagaaacac caccaattgt aatatttttct ggatctccac caaatttctc   1080

aatatttttct ttggtccatt tcaaagctgc tacctgatcc aataatccta catttccagg   1140

agcaccttcc aactccaaat tcaaaaatcc gagtggtccc aatcggtaat tgaaagttac   1200

aaaaataaca tcataattta ctaaataatc tgggctttga aattctaaat ttccggatcc   1260

agtcacaaaa ccgccaccat gaacccagaa aaatactgga agtttttttgt cagaagttgt   1320

ttttggtgcg tacacattca ccaacaagca gtcttcgtct ccttcaattt ttttcaagaa   1380
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gaaattcaaa gctttgcaca catttccatg tgatgtggcg ttgaaaacac cattccatgg 1440

ctcagctttc tgtggaggct taaatctaag ttctccaact ggaggtttag cataaggcac 1500

acctgtgtag ctaaaatact cttttccatt ttcgttcgtc aaagcttttc caaccaattc 1560

gccctggggc aaagttacag tcgggggatc acattttata aaattaaaac taaacaaaaa 1620

aatacaactt aaaaaaataa cacgagacat 1650

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<213> Ctenocephalides felis

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1               5                   10                  15

ttg acg aac gaa aat gga aaa gag tat ttt agc tac aca ggt gtg cct       96
Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr Thr Gly Val Pro
            20                  25                  30

tat gct aaa cct cca gtt gga gaa ctt aga ttt aag cct cca cag aaa      144
Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys Pro Pro Gln Lys
        35                  40                  45

gct gag cca tgg aat ggt gtt ttc aac gcc aca tca cat gga aat gtg      192
Ala Glu Pro Trp Asn Gly Val Phe Asn Ala Thr Ser His Gly Asn Val
    50                  55                  60

tgc aaa gct ttg aat ttc ttc ttg aaa aaa att gaa gga gac gaa gac      240
Cys Lys Ala Leu Asn Phe Phe Leu Lys Lys Ile Glu Gly Asp Glu Asp
65                  70                  75                  80

tgc ttg ttg gtg aat gtg tac gca cca aaa aca act tct gac aaa aaa      288
Cys Leu Leu Val Asn Val Tyr Ala Pro Lys Thr Thr Ser Asp Lys Lys
                85                  90                  95

ctt cca gta ttt ttc tgg gtt cat ggt ggc ggt ttt gtg act gga tcc      336
Leu Pro Val Phe Phe Trp Val His Gly Gly Gly Phe Val Thr Gly Ser
            100                 105                 110

gga aat tta gaa ttt caa agc cca gat tat tta gta aat tat gat gtt      384
Gly Asn Leu Glu Phe Gln Ser Pro Asp Tyr Leu Val Asn Tyr Asp Val
        115                 120                 125

att ttt gta act ttc aat tac cga ttg gga cca ctc gga ttt ttg aat      432
Ile Phe Val Thr Phe Asn Tyr Arg Leu Gly Pro Leu Gly Phe Leu Asn
    130                 135                 140

ttg gag ttg gaa ggt gct cct gga aat gta gga tta ttg gat cag gta      480
Leu Glu Leu Glu Gly Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Val
145                 150                 155                 160

gca gct ttg aaa tgg acc aaa gaa aat att gag aaa ttt ggt gga gat      528
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Ala Ala Leu Lys Trp Thr Lys Glu Asn Ile Glu Lys Phe Gly Gly Asp
                165                 170                 175

cca gaa aat att aca att ggt ggt gtt tct gct ggt gga gca agt gtt      576
Pro Glu Asn Ile Thr Ile Gly Gly Val Ser Ala Gly Gly Ala Ser Val
            180                 185                 190

cat tat ctt tta ttg tca cat aca acc act gga ctt tac aaa agg gca      624
His Tyr Leu Leu Leu Ser His Thr Thr Thr Gly Leu Tyr Lys Arg Ala
        195                 200                 205

att gct caa agt gga agt gct tta aat cca tgg gcc ttc caa aga cat      672
Ile Ala Gln Ser Gly Ser Ala Leu Asn Pro Trp Ala Phe Gln Arg His
    210                 215                 220

cca gta aag cgt agt ctt caa ctt gct gag ata tta ggt cat ccc aca      720
Pro Val Lys Arg Ser Leu Gln Leu Ala Glu Ile Leu Gly His Pro Thr
225                 230                 235                 240

aac aac act caa gat gct tta gaa ttc tta caa aaa gcc cca gta gac      768
Asn Asn Thr Gln Asp Ala Leu Glu Phe Leu Gln Lys Ala Pro Val Asp
                245                 250                 255

agt ctc ctg aaa aaa atg cca gct gaa aca gaa ggt gaa ata ata gaa      816
Ser Leu Leu Lys Lys Met Pro Ala Glu Thr Glu Gly Glu Ile Ile Glu
            260                 265                 270

gag ttc gtc ttc gta cca tca att gaa aaa gtt ttc cca tcc cac caa      864
Glu Phe Val Phe Val Pro Ser Ile Glu Lys Val Phe Pro Ser His Gln
        275                 280                 285

cct ttc ttg gaa gaa tca cca ttg gcc aga atg aaa tct gga tcc ttt      912
Pro Phe Leu Glu Glu Ser Pro Leu Ala Arg Met Lys Ser Gly Ser Phe
    290                 295                 300

aac aaa gta cct tta tta gtt gga ttc aac agc gca gaa gga ctt ttg      960
Asn Lys Val Pro Leu Leu Val Gly Phe Asn Ser Ala Glu Gly Leu Leu
305                 310                 315                 320

tac aaa ttc ttt atg aaa gaa aaa cca gag atg ctg aac caa gct gaa     1008
Tyr Lys Phe Phe Met Lys Glu Lys Pro Glu Met Leu Asn Gln Ala Glu
                325                 330                 335

gca gat ttc gaa aga ctc gta cca gcc gaa ttt gaa tta gcc cat gga     1056
Ala Asp Phe Glu Arg Leu Val Pro Ala Glu Phe Glu Leu Ala His Gly
            340                 345                 350

tca gaa gaa tcg aaa aaa ctt gca gaa aaa atc agg aag ttt tac ttt     1104
Ser Glu Glu Ser Lys Lys Leu Ala Glu Lys Ile Arg Lys Phe Tyr Phe
        355                 360                 365

gac gat aaa ccc gtt cct gaa aat gag cag aaa ttt att gac ttg ata     1152
Asp Asp Lys Pro Val Pro Glu Asn Glu Gln Lys Phe Ile Asp Leu Ile
    370                 375                 380

gga gat att tgg ttt act aga ggc att gac aag cat gtc aag ttg tct     1200
Gly Asp Ile Trp Phe Thr Arg Gly Ile Asp Lys His Val Lys Leu Ser
385                 390                 395                 400

gta gaa aaa caa gac gag cca gta tat tat tat gaa tat tct ttc tct     1248
Val Glu Lys Gln Asp Glu Pro Val Tyr Tyr Tyr Glu Tyr Ser Phe Ser
                405                 410                 415

gaa agt cat cct gca aaa gga aca ttt ggt gac cat aac ttg act gga     1296
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Glu Ser His Pro Ala Lys Gly Thr Phe Gly Asp His Asn Leu Thr Gly
            420                 425                 430

gca tgt cat ggt gaa gaa ctt gtg aat tta ttc aaa gtc gag atg atg     1344
Ala Cys His Gly Glu Glu Leu Val Asn Leu Phe Lys Val Glu Met Met
        435                 440                 445

aag ctg gaa aaa gat aaa ccg aat gtt tta tta aca aaa gat agg gta     1392
Lys Leu Glu Lys Asp Lys Pro Asn Val Leu Leu Thr Lys Asp Arg Val
    450                 455                 460

ctt gct atg tgg acg aac ttc atc aaa aat gga aat cct act cct gaa     1440
Leu Ala Met Trp Thr Asn Phe Ile Lys Asn Gly Asn Pro Thr Pro Glu
465                 470                 475                 480

gta act gaa tta ttg cca gtt aaa tgg gaa cct gcc aca aaa gac aag     1488
Val Thr Glu Leu Leu Pro Val Lys Trp Glu Pro Ala Thr Lys Asp Lys
                485                 490                 495

ttg aat tat ttg aac att gat gcc acc tta act ttg gga aca aat cca     1536
Leu Asn Tyr Leu Asn Ile Asp Ala Thr Leu Thr Leu Gly Thr Asn Pro
            500                 505                 510

gaa gaa acc cga gtc aaa tty tgg gaa gat gcc aca aaa act ttg cac     1584
Glu Glu Thr Arg Val Lys Phe Trp Glu Asp Ala Thr Lys Thr Leu His
        515                 520                 525

agt caa                                                            1590
Ser Gln
    530
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<210> 24
<211> 2836
<212> DNA
<213> Ctenocephalides felis

<220>
<221> CDS
<222> (99)..(1889)
<223>

<220>
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<222> (2278)..(2278)
<223> n = unknown

<400> 24

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                                        Met Leu Pro His Ser Ser
                                        1               5

gca tta gtt tta ttt tta ttt ttt tta ttt ttc tta ttt aca cct atc      164
Ala Leu Val Leu Phe Leu Phe Phe Leu Phe Phe Leu Phe Thr Pro Ile
            10                  15                  20

ttg tgc ata cta tgg gat aac cta gat cag cat ttg tgc aga gtt caa      212
Leu Cys Ile Leu Trp Asp Asn Leu Asp Gln His Leu Cys Arg Val Gln
        25                  30                  35
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ttt aac ggg atc acg gaa gga aaa ccg ttc cga tat aaa gat cat agg      260
Phe Asn Gly Ile Thr Glu Gly Lys Pro Phe Arg Tyr Lys Asp His Arg
    40                  45                  50

aat gat gta tat tgt tct tat ttg gga att cct tat gcc gaa ccg cct      308
Asn Asp Val Tyr Cys Ser Tyr Leu Gly Ile Pro Tyr Ala Glu Pro Pro
55                  60                  65                  70

ttt gga cca tta cga ttt cag tct cca aaa cca ata tca aat cca aaa      356
Phe Gly Pro Leu Arg Phe Gln Ser Pro Lys Pro Ile Ser Asn Pro Lys
                75                  80                  85

aca gga ttc gta cag gct cga act ttg gga gac aaa tgt ttc cag gaa      404
Thr Gly Phe Val Gln Ala Arg Thr Leu Gly Asp Lys Cys Phe Gln Glu
            90                  95                  100

agt cta ata tat tct tat gca gga agc gaa gat tgc tta tat ctg aat      452
Ser Leu Ile Tyr Ser Tyr Ala Gly Ser Glu Asp Cys Leu Tyr Leu Asn
        105                 110                 115

ata ttc acg cca gag act gtt aat tct gcg aac aat aca aaa tat cct      500
Ile Phe Thr Pro Glu Thr Val Asn Ser Ala Asn Asn Thr Lys Tyr Pro
    120                 125                 130

gta atg ttc tgg atc cat gga ggc gca ttc aac caa gga tca gga tct      548
Val Met Phe Trp Ile His Gly Gly Ala Phe Asn Gln Gly Ser Gly Ser
135                 140                 145                 150

tat aat ttt ttt gga cct gat tat ttg atc agg gaa gga att att ttg      596
Tyr Asn Phe Phe Gly Pro Asp Tyr Leu Ile Arg Glu Gly Ile Ile Leu
                155                 160                 165

gtc act atc aac tat aga tta gga gtt ttc ggt ttt cta tca gcg ccg      644
Val Thr Ile Asn Tyr Arg Leu Gly Val Phe Gly Phe Leu Ser Ala Pro
            170                 175                 180

gaa tgg gat atc cat gga aat atg ggt cta aaa gac cag aga ttg gca      692
Glu Trp Asp Ile His Gly Asn Met Gly Leu Lys Asp Gln Arg Leu Ala
        185                 190                 195

cta aaa tgg gtt tac gac aac atc gaa aag ttt ggt gga gac aga gaa      740
Leu Lys Trp Val Tyr Asp Asn Ile Glu Lys Phe Gly Gly Asp Arg Glu
    200                 205                 210

aaa att aca att gct gga gaa tct gct gga gca gca agt gtc cat ttt      788
Lys Ile Thr Ile Ala Gly Glu Ser Ala Gly Ala Ala Ser Val His Phe
215                 220                 225                 230

ctg atg atg gac aac tcg act aga aaa tac tac caa agg gcc att ttg      836
Leu Met Met Asp Asn Ser Thr Arg Lys Tyr Tyr Gln Arg Ala Ile Leu
                235                 240                 245

cag agt ggg aca tta cta aat ccg act gct aat caa att caa ctt ctg      884
Gln Ser Gly Thr Leu Leu Asn Pro Thr Ala Asn Gln Ile Gln Leu Leu
            250                 255                 260

cat aga ttt gaa aaa ctc aaa caa gtg cta aac atc acg caa aaa caa      932
His Arg Phe Glu Lys Leu Lys Gln Val Leu Asn Ile Thr Gln Lys Gln
        265                 270                 275

gaa ctc cta aac ctg gat aaa aac cta att tta cga gca gcc tta aac      980
Glu Leu Leu Asn Leu Asp Lys Asn Leu Ile Leu Arg Ala Ala Leu Asn
    280                 285                 290
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aga gtt cct gat agc aac gac cat gac cga gac aca gta cca gta ttt      1028
Arg Val Pro Asp Ser Asn Asp His Asp Arg Asp Thr Val Pro Val Phe
295                 300                 305                 310

aat cca gtc tta gaa tca cca gaa tct cca gat cca ata aca ttt cca      1076
Asn Pro Val Leu Glu Ser Pro Glu Ser Pro Asp Pro Ile Thr Phe Pro
                315                 320                 325

tct gcc ttg gaa aga atg aga aat ggt gaa ttt cct gat gtc gat gtc      1124
Ser Ala Leu Glu Arg Met Arg Asn Gly Glu Phe Pro Asp Val Asp Val
            330                 335                 340

atc att ggt ttc aat agt gct gaa ggt tta aga tct atg gca aga gta      1172
Ile Ile Gly Phe Asn Ser Ala Glu Gly Leu Arg Ser Met Ala Arg Val
        345                 350                 355

acc aga gga aac atg gaa gtt cac aag act ttg aca aat ata gaa agg      1220
Thr Arg Gly Asn Met Glu Val His Lys Thr Leu Thr Asn Ile Glu Arg
    360                 365                 370

gct ata cct aga gat gct aat att tgg aaa aat cca aat ggt att gag      1268
Ala Ile Pro Arg Asp Ala Asn Ile Trp Lys Asn Pro Asn Gly Ile Glu
375                 380                 385                 390

gag aaa aaa cta ata aaa atg ctt aca gag ttt tat gac caa gtg aaa      1316
Glu Lys Lys Leu Ile Lys Met Leu Thr Glu Phe Tyr Asp Gln Val Lys
                395                 400                 405

gaa caa aac gat gac att gaa gcc tac gtc caa cta aaa ggc gat gct      1364
Glu Gln Asn Asp Asp Ile Glu Ala Tyr Val Gln Leu Lys Gly Asp Ala
            410                 415                 420

ggt tac ctc caa gga atc tac cgt acc ttg aaa gcc ata ttt ttc aat      1412
Gly Tyr Leu Gln Gly Ile Tyr Arg Thr Leu Lys Ala Ile Phe Phe Asn
        425                 430                 435

gaa ttc aga agg aat tcc aat ttg tat ttg tac agg tta tca gac gat      1460
Glu Phe Arg Arg Asn Ser Asn Leu Tyr Leu Tyr Arg Leu Ser Asp Asp
    440                 445                 450

acg tat agt gta tat aaa agt tat atc ttg ccc tat cga tgg ggt tcc      1508
Thr Tyr Ser Val Tyr Lys Ser Tyr Ile Leu Pro Tyr Arg Trp Gly Ser
455                 460                 465                 470

ttg cca gga gtt agt cat ggt gat gat tta gga tat ctt ttt gca aac      1556
Leu Pro Gly Val Ser His Gly Asp Asp Leu Gly Tyr Leu Phe Ala Asn
                475                 480                 485

tcg ttg gat gtt cct att ttg gga aca acg cac att tct ata ccg caa      1604
Ser Leu Asp Val Pro Ile Leu Gly Thr Thr His Ile Ser Ile Pro Gln
            490                 495                 500

gat gct atg cag act ctg gaa agg atg gtc agg atc tgg acc aat ttt      1652
Asp Ala Met Gln Thr Leu Glu Arg Met Val Arg Ile Trp Thr Asn Phe
        505                 510                 515

gta aag aat gga aaa cct aca tca aac act gaa gat gca tca tgt gat      1700
Val Lys Asn Gly Lys Pro Thr Ser Asn Thr Glu Asp Ala Ser Cys Asp
    520                 525                 530

aca aaa aga cat tta aac gac att ttt tgg gaa cca tac aac gac gaa      1748
Thr Lys Arg His Leu Asn Asp Ile Phe Trp Glu Pro Tyr Asn Asp Glu
535                 540                 545                 550
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gaa cca aaa tat ttg gac atg gga aaa gaa aat ttt gaa atg aaa aat      1796
Glu Pro Lys Tyr Leu Asp Met Gly Lys Glu Asn Phe Glu Met Lys Asn
                555                 560                 565

att ttg gaa cta aaa cgc atg atg ctt tgg gat gaa gtt tat aga aat      1844
Ile Leu Glu Leu Lys Arg Met Met Leu Trp Asp Glu Val Tyr Arg Asn
            570                 575                 580

gcg aat ttg cgg ttt aga gtc tgt aat gaa gaa agt att aga tga          1889
Ala Asn Leu Arg Phe Arg Val Cys Asn Glu Glu Ser Ile Arg
        585                 590                 595

gttttttttaa ttttacatac agccgagagg aaacatgact aaaattggaa agaaaaatca   1949

gaaaaagaaa aatcacatgg accatagtaa ctttattaca tgatttagtt tcaagtgtat   2009

caagaaaact tattgcatca aagaaaatat tattttgcca aaattcttgg aaaaacactt   2069

tttatgactg acatggccca taattgaagc ttttttcttct tttaccaaat cgccaaattt   2129

tgtagcgtca gacacattta tttatgacat ggcaattaat gtgttaaaca ttcaactcta   2189

tattaaaaat ggtagtattt tctaataaga aggttatata aaaagacttg aaaataataa   2249

gatttgctcg gctatatata aaaacttanc gtctcgttat gctaaacttt tttgatggta   2309

aaaatatgtt gattttccta ataatctaag atattatatt ttagattaaa ttaaaatatg   2369

atattttcaa ttaattaatt ttagttttaa atgtactata tttaccagta ctatgaaact   2429

attttaaata tatttttttat tacaatattt atttctcaaa aatgtttagt gtaacaagac   2489

cattaaatta gagttaatgt tgtaaattaa actatttttt atctatcaca accgcttaat   2549

tggtgcaaag aaaaatttta ctgtgataat atttgacatt tacacaatat tacgaattgt   2609

aaactcacaa ttatgtgaat attgtttttt gttaaaaaaa catacatgac ttttctatat   2669

cattttatat tacggtgata tggattaatg tcaacatgta aaatacaaat gcggttgtta   2729

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                  2836
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Phe Leu Phe Thr Pro Ile Leu Cys Ile Leu Trp Asp Asn Leu Asp Gln
            20                  25                  30

His Leu Cys Arg Val Gln Phe Asn Gly Ile Thr Glu Gly Lys Pro Phe
        35                  40                  45
```

```
Arg Tyr Lys Asp His Arg Asn Asp Val Tyr Cys Ser Tyr Leu Gly Ile
    50                  55                  60

Pro Tyr Ala Glu Pro Pro Phe Gly Pro Leu Arg Phe Gln Ser Pro Lys
65                  70                  75                  80

Pro Ile Ser Asn Pro Lys Thr Gly Phe Val Gln Ala Arg Thr Leu Gly
                85                  90                  95

Asp Lys Cys Phe Gln Glu Ser Leu Ile Tyr Ser Tyr Ala Gly Ser Glu
            100                 105                 110

Asp Cys Leu Tyr Leu Asn Ile Phe Thr Pro Glu Thr Val Asn Ser Ala
        115                 120                 125

Asn Asn Thr Lys Tyr Pro Val Met Phe Trp Ile His Gly Gly Ala Phe
    130                 135                 140

Asn Gln Gly Ser Gly Ser Tyr Asn Phe Phe Gly Pro Asp Tyr Leu Ile
145                 150                 155                 160

Arg Glu Gly Ile Ile Leu Val Thr Ile Asn Tyr Arg Leu Gly Val Phe
                165                 170                 175

Gly Phe Leu Ser Ala Pro Glu Trp Asp Ile His Gly Asn Met Gly Leu
            180                 185                 190

Lys Asp Gln Arg Leu Ala Leu Lys Trp Val Tyr Asp Asn Ile Glu Lys
        195                 200                 205

Phe Gly Gly Asp Arg Glu Lys Ile Thr Ile Ala Gly Glu Ser Ala Gly
    210                 215                 220

Ala Ala Ser Val His Phe Leu Met Met Asp Asn Ser Thr Arg Lys Tyr
225                 230                 235                 240

Tyr Gln Arg Ala Ile Leu Gln Ser Gly Thr Leu Leu Asn Pro Thr Ala
                245                 250                 255

Asn Gln Ile Gln Leu Leu His Arg Phe Glu Lys Leu Lys Gln Val Leu
            260                 265                 270

Asn Ile Thr Gln Lys Gln Glu Leu Leu Asn Leu Asp Lys Asn Leu Ile
        275                 280                 285

Leu Arg Ala Ala Leu Asn Arg Val Pro Asp Ser Asn Asp His Asp Arg
    290                 295                 300
```

```
Asp Thr Val Pro Val Phe Asn Pro Val Leu Glu Ser Pro Glu Ser Pro
305                 310                 315                 320

Asp Pro Ile Thr Phe Pro Ser Ala Leu Glu Arg Met Arg Asn Gly Glu
                325                 330                 335

Phe Pro Asp Val Asp Val Ile Ile Gly Phe Asn Ser Ala Glu Gly Leu
            340                 345                 350

Arg Ser Met Ala Arg Val Thr Arg Gly Asn Met Glu Val His Lys Thr
        355                 360                 365

Leu Thr Asn Ile Glu Arg Ala Ile Pro Arg Asp Ala Asn Ile Trp Lys
    370                 375                 380

Asn Pro Asn Gly Ile Glu Glu Lys Lys Leu Ile Lys Met Leu Thr Glu
385                 390                 395                 400

Phe Tyr Asp Gln Val Lys Glu Gln Asn Asp Asp Ile Glu Ala Tyr Val
                405                 410                 415

Gln Leu Lys Gly Asp Ala Gly Tyr Leu Gln Gly Ile Tyr Arg Thr Leu
            420                 425                 430

Lys Ala Ile Phe Phe Asn Glu Phe Arg Arg Asn Ser Asn Leu Tyr Leu
        435                 440                 445

Tyr Arg Leu Ser Asp Asp Thr Tyr Ser Val Tyr Lys Ser Tyr Ile Leu
    450                 455                 460

Pro Tyr Arg Trp Gly Ser Leu Pro Gly Val Ser His Gly Asp Asp Leu
465                 470                 475                 480

Gly Tyr Leu Phe Ala Asn Ser Leu Asp Val Pro Ile Leu Gly Thr Thr
                485                 490                 495

His Ile Ser Ile Pro Gln Asp Ala Met Gln Thr Leu Glu Arg Met Val
            500                 505                 510

Arg Ile Trp Thr Asn Phe Val Lys Asn Gly Lys Pro Thr Ser Asn Thr
        515                 520                 525

Glu Asp Ala Ser Cys Asp Thr Lys Arg His Leu Asn Asp Ile Phe Trp
    530                 535                 540

Glu Pro Tyr Asn Asp Glu Glu Pro Lys Tyr Leu Asp Met Gly Lys Glu
545                 550                 555                 560
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Asn Phe Glu Met Lys Asn Ile Leu Glu Leu Lys Arg Met Met Leu Trp
565 570 575

Asp Glu Val Tyr Arg Asn Ala Asn Leu Arg Phe Arg Val Cys Asn Glu
580 585 590

Glu Ser Ile Arg
595

<210> 26
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<213> Ctenocephalides felis

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tgtattttac atgttgacat taatccatat caccgtaata taaaatgata tagaaaagtc 180

atgtatgttt ttttaacaaa aaacaatatt cacataattg tgagtttaca attcgtaata 240

ttgtgtaaat gtcaaatatt atcacagtaa aatttttctt tgcaccaatt aagcggttgt 300

gatagataaa aaatagttta atttacaaca ttaactctaa tttaatggtc ttgttacact 360

aaacattttt gagaaataaa tattgtaata aaaaatatat ttaaaatagt ttcatagtac 420

tggtaaatat agtacattta aaactaaaat taattaattg aaaatatcat attttaattt 480

aatctaaaat ataatatctt agattattag gaaaatcaac atatttttac catcaaaaaa 540

gtttagcata acgagacgnt aagtttttat atatagccga gcaaatctta ttattttcaa 600

gtctttttat ataaccttct tattagaaaa tactaccatt tttaatatag agttgaatgt 660

ttaacacatt aattgccatg tcataaataa atgtgtctga cgctacaaaa tttggcgatt 720

tggtaaaaga agaaaaagct tcaattatgg gccatgtcag tcataaaaag tgtttttcca 780

agaattttgg caaaataata ttttctttga tgcaataagt tttcttgata cacttgaaac 840

taaatcatgt aataaagtta ctatggtcca tgtgattttt ctttttctga tttttctttc 900

caattttagt catgtttcct ctcggctgta tgtaaaatta aaaaaactca tctaatactt 960

tcttcattac agactctaaa ccgcaaattc gcatttctat aaacttcatc ccaaagcatc 1020

atgcgtttta gttccaaaat atttttcatt tcaaaatttt cttttcccat gtccaaatat 1080

tttggttctt cgtcgttgta tggttcccaa aaaatgtcgt ttaaatgtct ttttgtatca 1140

catgatgcat cttcagtgtt tgatgtaggt tttccattct ttacaaaatt ggtccagatc 1200

ctgaccatcc tttccagagt ctgcatagca tcttgcggta tagaaatgtg cgttgttccc 1260

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cctggcaagg aaccccatcg atagggcaag atataacttt tatatacact atacgtatcg 1380

tctgataacc tgtacaaata caaattggaa ttccttctga attcattgaa aaatatggct 1440

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actggattaa atactggtac tgtgtctcgg tcatggtcgt tgctatcagg aactctgttt 1860

aaggctgctc gtaaaattag gtttttatcc aggtttagga gttcttgttt ttgcgtgatg 1920

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tttagtaatg tcccactctg caaaatggcc ctttggtagt attttctagt cgagttgtcc 2040

atcatcagaa aatggacact tgctgctcca gcagattctc cagcaattgt aatttttttct 2100

ctgtctccac caaacttttc gatgttgtcg taaacccatt ttagtgccaa tctctggtct 2160

tttagaccca tatttccatg gatatcccat tccggcgctg atagaaaacc gaaaactcct 2220

aatctatagt tgatagtgac caaaataatt ccttccctga tcaaataatc aggtccaaaa 2280

aaattataag atcctgatcc ttggttgaat gcgcctccat ggatccagaa cattacagga 2340

tattttgtat tgttcgcaga attaacagtc tctggcgtga atatattcag atataagcaa 2400

tcttcgcttc ctgcataaga atatattaga ctttcctgga aacatttgtc tcccaaagtt 2460

cgagcctgta cgaatcctgt ttttggattt gatattggtt ttggagactg aaatcgtaat 2520

ggtccaaaag gcggttcggc ataaggaatt cccaaataag aacaatatac atcattccta 2580

tgatctttat atcggaacgg ttttccttcc gtgatcccgt taaattgaac tctgcacaaa 2640

tgctgatcta ggttatccca tagtatgcac aagataggtg taaataagaa aaataaaaaa 2700

aataaaaata aaactaatgc actactgtga ggtaacattt tttattgtgt tttttaatgc 2760

attttggttg cttaattgtt attatttatc tcgttttgtt tatgataaaa tagacgtttt 2820

gaagacgaca tgtcta 2836

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1               5                  10                  15

acg gaa gga aaa ccg ttc cga tat aaa gat cat agg aat gat gta tat        96
Thr Glu Gly Lys Pro Phe Arg Tyr Lys Asp His Arg Asn Asp Val Tyr
            20                  25                  30

tgt tct tat ttg gga att cct tat gcc gaa ccg cct ttt gga cca tta       144
Cys Ser Tyr Leu Gly Ile Pro Tyr Ala Glu Pro Pro Phe Gly Pro Leu
        35                  40                  45

cga ttt cag tct cca aaa cca ata tca aat cca aaa aca gga ttc gta       192
Arg Phe Gln Ser Pro Lys Pro Ile Ser Asn Pro Lys Thr Gly Phe Val
    50                  55                  60

cag gct cga act ttg gga gac aaa tgt ttc cag gaa agt cta ata tat       240
Gln Ala Arg Thr Leu Gly Asp Lys Cys Phe Gln Glu Ser Leu Ile Tyr
65                  70                  75                  80

tct tat gca gga agc gaa gat tgc tta tat ctg aat ata ttc acg cca       288
Ser Tyr Ala Gly Ser Glu Asp Cys Leu Tyr Leu Asn Ile Phe Thr Pro
                85                  90                  95

gag act gtt aat tct gcg aac aat aca aaa tat cct gta atg ttc tgg       336
Glu Thr Val Asn Ser Ala Asn Asn Thr Lys Tyr Pro Val Met Phe Trp
            100                 105                 110

atc cat gga ggc gca ttc aac caa gga tca gga tct tat aat ttt ttt       384
Ile His Gly Gly Ala Phe Asn Gln Gly Ser Gly Ser Tyr Asn Phe Phe
        115                 120                 125

gga cct gat tat ttg atc agg gaa gga att att ttg gtc act atc aac       432
Gly Pro Asp Tyr Leu Ile Arg Glu Gly Ile Ile Leu Val Thr Ile Asn
    130                 135                 140

tat aga tta gga gtt ttc ggt ttt cta tca gcg ccg gaa tgg gat atc       480
Tyr Arg Leu Gly Val Phe Gly Phe Leu Ser Ala Pro Glu Trp Asp Ile
145                 150                 155                 160

cat gga aat atg ggt cta aaa gac cag aga ttg gca cta aaa tgg gtt       528
His Gly Asn Met Gly Leu Lys Asp Gln Arg Leu Ala Leu Lys Trp Val
                165                 170                 175

tac gac aac atc gaa aag ttt ggt gga gac aga gaa aaa att aca att       576
Tyr Asp Asn Ile Glu Lys Phe Gly Gly Asp Arg Glu Lys Ile Thr Ile
            180                 185                 190

gct gga gaa tct gct gga gca gca agt gtc cat ttt ctg atg atg gac       624
Ala Gly Glu Ser Ala Gly Ala Ala Ser Val His Phe Leu Met Met Asp
        195                 200                 205

aac tcg act aga aaa tac tac caa agg gcc att ttg cag agt ggg aca       672
Asn Ser Thr Arg Lys Tyr Tyr Gln Arg Ala Ile Leu Gln Ser Gly Thr
    210                 215                 220

tta cta aat ccg act gct aat caa att caa ctt ctg cat aga ttt gaa       720
Leu Leu Asn Pro Thr Ala Asn Gln Ile Gln Leu Leu His Arg Phe Glu
225                 230                 235                 240
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aaa ctc aaa caa gtg cta aac atc acg caa aaa caa gaa ctc cta aac      768
Lys Leu Lys Gln Val Leu Asn Ile Thr Gln Lys Gln Glu Leu Leu Asn
                245                 250                 255

ctg gat aaa aac cta att tta cga gca gcc tta aac aga gtt cct gat      816
Leu Asp Lys Asn Leu Ile Leu Arg Ala Ala Leu Asn Arg Val Pro Asp
            260                 265                 270

agc aac gac cat gac cga gac aca gta cca gta ttt aat cca gtc tta      864
Ser Asn Asp His Asp Arg Asp Thr Val Pro Val Phe Asn Pro Val Leu
        275                 280                 285

gaa tca cca gaa tct cca gat cca ata aca ttt cca tct gcc ttg gaa      912
Glu Ser Pro Glu Ser Pro Asp Pro Ile Thr Phe Pro Ser Ala Leu Glu
    290                 295                 300

aga atg aga aat ggt gaa ttt cct gat gtc gat gtc atc att ggt ttc      960
Arg Met Arg Asn Gly Glu Phe Pro Asp Val Asp Val Ile Ile Gly Phe
305                 310                 315                 320

aat agt gct gaa ggt tta aga tct atg gca aga gta acc aga gga aac     1008
Asn Ser Ala Glu Gly Leu Arg Ser Met Ala Arg Val Thr Arg Gly Asn
                325                 330                 335

atg gaa gtt cac aag act ttg aca aat ata gaa agg gct ata cct aga     1056
Met Glu Val His Lys Thr Leu Thr Asn Ile Glu Arg Ala Ile Pro Arg
            340                 345                 350

gat gct aat att tgg aaa aat cca aat ggt att gag gag aaa aaa cta     1104
Asp Ala Asn Ile Trp Lys Asn Pro Asn Gly Ile Glu Glu Lys Lys Leu
        355                 360                 365

ata aaa atg ctt aca gag ttt tat gac caa gtg aaa gaa caa aac gat     1152
Ile Lys Met Leu Thr Glu Phe Tyr Asp Gln Val Lys Glu Gln Asn Asp
    370                 375                 380

gac att gaa gcc tac gtc caa cta aaa ggc gat gct ggt tac ctc caa     1200
Asp Ile Glu Ala Tyr Val Gln Leu Lys Gly Asp Ala Gly Tyr Leu Gln
385                 390                 395                 400

gga atc tac cgt acc ttg aaa gcc ata ttt ttc aat gaa ttc aga agg     1248
Gly Ile Tyr Arg Thr Leu Lys Ala Ile Phe Phe Asn Glu Phe Arg Arg
                405                 410                 415

aat tcc aat ttg tat ttg tac agg tta tca gac gat acg tat agt gta     1296
Asn Ser Asn Leu Tyr Leu Tyr Arg Leu Ser Asp Asp Thr Tyr Ser Val
            420                 425                 430

tat aaa agt tat atc ttg ccc tat cga tgg ggt tcc ttg cca gga gtt     1344
Tyr Lys Ser Tyr Ile Leu Pro Tyr Arg Trp Gly Ser Leu Pro Gly Val
        435                 440                 445

agt cat ggt gat gat tta gga tat ctt ttt gca aac tcg ttg gat gtt     1392
Ser His Gly Asp Asp Leu Gly Tyr Leu Phe Ala Asn Ser Leu Asp Val
    450                 455                 460

cct att ttg gga aca acg cac att tct ata ccg caa gat gct atg cag     1440
Pro Ile Leu Gly Thr Thr His Ile Ser Ile Pro Gln Asp Ala Met Gln
465                 470                 475                 480

act ctg gaa agg atg gtc agg atc tgg acc aat ttt gta aag aat gga     1488
Thr Leu Glu Arg Met Val Arg Ile Trp Thr Asn Phe Val Lys Asn Gly
                485                 490                 495
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```
aaa cct aca tca aac act gaa gat gca tca tgt gat aca aaa aga cat     1536
Lys Pro Thr Ser Asn Thr Glu Asp Ala Ser Cys Asp Thr Lys Arg His
            500                 505                 510

tta aac gac att ttt tgg gaa cca tac aac gac gaa gaa cca aaa tat     1584
Leu Asn Asp Ile Phe Trp Glu Pro Tyr Asn Asp Glu Glu Pro Lys Tyr
        515                 520                 525

ttg gac atg gga aaa gaa aat ttt gaa atg aaa aat att ttg gaa cta     1632
Leu Asp Met Gly Lys Glu Asn Phe Glu Met Lys Asn Ile Leu Glu Leu
    530                 535                 540

aaa cgc atg atg ctt tgg gat gaa gtt tat aga aat gcg aat ttg cgg     1680
Lys Arg Met Met Leu Trp Asp Glu Val Tyr Arg Asn Ala Asn Leu Arg
545                 550                 555                 560

ttt aga gtc tgt aat gaa gaa agt att aga                            1710
Phe Arg Val Cys Asn Glu Glu Ser Ile Arg
                565                 570
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<210> 28
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<220>
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<400> 28

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Met Leu Pro His Ser Ser Ala Leu Val Leu Phe Leu Phe Phe Leu Phe
1               5                   10                  15

ttc tta ttt aca cct atc ttg tgc ata cta tgg gat aac cta gat cag      96
Phe Leu Phe Thr Pro Ile Leu Cys Ile Leu Trp Asp Asn Leu Asp Gln
            20                  25                  30

cat ttg tgc aga gtt caa ttt aac ggg atc acg gaa gga aaa ccg ttc     144
His Leu Cys Arg Val Gln Phe Asn Gly Ile Thr Glu Gly Lys Pro Phe
        35                  40                  45

cga tat aaa gat cat agg aat gat gta tat tgt tct tat ttg gga att     192
Arg Tyr Lys Asp His Arg Asn Asp Val Tyr Cys Ser Tyr Leu Gly Ile
    50                  55                  60

cct tat gcc gaa ccg cct ttt gga cca tta cga ttt cag tct cca aaa     240
Pro Tyr Ala Glu Pro Pro Phe Gly Pro Leu Arg Phe Gln Ser Pro Lys
65                  70                  75                  80

cca ata tca aat cca aaa aca gga ttc gta cag gct cga act ttg gga     288
Pro Ile Ser Asn Pro Lys Thr Gly Phe Val Gln Ala Arg Thr Leu Gly
                85                  90                  95

gac aaa tgt ttc cag gaa agt cta ata tat tct tat gca gga agc gaa     336
Asp Lys Cys Phe Gln Glu Ser Leu Ile Tyr Ser Tyr Ala Gly Ser Glu
            100                 105                 110

gat tgc tta tat ctg aat ata ttc acg cca gag act gtt aat tct gcg     384
Asp Cys Leu Tyr Leu Asn Ile Phe Thr Pro Glu Thr Val Asn Ser Ala
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```
        115                 120                 125

aac aat aca aaa tat cct gta atg ttc tgg atc cat gga ggc gca ttc      432
Asn Asn Thr Lys Tyr Pro Val Met Phe Trp Ile His Gly Gly Ala Phe
    130                 135                 140

aac caa gga tca gga tct tat aat ttt ttt gga cct gat tat ttg atc      480
Asn Gln Gly Ser Gly Ser Tyr Asn Phe Phe Gly Pro Asp Tyr Leu Ile
145                 150                 155                 160

agg gaa gga att att ttg gtc act atc aac tat aga tta gga gtt ttc      528
Arg Glu Gly Ile Ile Leu Val Thr Ile Asn Tyr Arg Leu Gly Val Phe
                165                 170                 175

ggt ttt cta tca gcg ccg gaa tgg gat atc cat gga aat atg ggt cta      576
Gly Phe Leu Ser Ala Pro Glu Trp Asp Ile His Gly Asn Met Gly Leu
            180                 185                 190

aaa gac cag aga ttg gca cta aaa tgg gtt tac gac aac atc gaa aag      624
Lys Asp Gln Arg Leu Ala Leu Lys Trp Val Tyr Asp Asn Ile Glu Lys
        195                 200                 205

ttt ggt gga gac aga gaa aaa att aca att gct gga gaa tct gct gga      672
Phe Gly Gly Asp Arg Glu Lys Ile Thr Ile Ala Gly Glu Ser Ala Gly
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gca gca agt gtc cat ttt ctg atg atg gac aac tcg act aga aaa tac      720
Ala Ala Ser Val His Phe Leu Met Met Asp Asn Ser Thr Arg Lys Tyr
225                 230                 235                 240

tac caa agg gcc att ttg cag agt ggg aca tta cta aat ccg act gct      768
Tyr Gln Arg Ala Ile Leu Gln Ser Gly Thr Leu Leu Asn Pro Thr Ala
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aat caa att caa ctt ctg cat aga ttt gaa aaa ctc aaa caa gtg cta      816
Asn Gln Ile Gln Leu Leu His Arg Phe Glu Lys Leu Lys Gln Val Leu
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aac atc acg caa aaa caa gaa ctc cta aac ctg gat aaa aac cta att      864
Asn Ile Thr Gln Lys Gln Glu Leu Leu Asn Leu Asp Lys Asn Leu Ile
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tta cga gca gcc tta aac aga gtt cct gat agc aac gac cat gac cga      912
Leu Arg Ala Ala Leu Asn Arg Val Pro Asp Ser Asn Asp His Asp Arg
    290                 295                 300

gac aca gta cca gta ttt aat cca gtc tta gaa tca cca gaa tct cca      960
Asp Thr Val Pro Val Phe Asn Pro Val Leu Glu Ser Pro Glu Ser Pro
305                 310                 315                 320

gat cca ata aca ttt cca tct gcc ttg gaa aga atg aga aat ggt gaa     1008
Asp Pro Ile Thr Phe Pro Ser Ala Leu Glu Arg Met Arg Asn Gly Glu
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ttt cct gat gtc gat gtc atc att ggt ttc aat agt gct gaa ggt tta     1056
Phe Pro Asp Val Asp Val Ile Ile Gly Phe Asn Ser Ala Glu Gly Leu
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aga tct atg gca aga gta acc aga gga aac atg gaa gtt cac aag act     1104
Arg Ser Met Ala Arg Val Thr Arg Gly Asn Met Glu Val His Lys Thr
        355                 360                 365

ttg aca aat ata gaa agg gct ata cct aga gat gct aat att tgg aaa     1152
Leu Thr Asn Ile Glu Arg Ala Ile Pro Arg Asp Ala Asn Ile Trp Lys
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370                 375                 380

aat cca aat ggt att gag gag aaa aaa cta ata aaa atg ctt aca gag     1200
Asn Pro Asn Gly Ile Glu Glu Lys Lys Leu Ile Lys Met Leu Thr Glu
385                 390                 395                 400

ttt tat gac caa gtg aaa gaa caa aac gat gac att gaa gcc tac gtc     1248
Phe Tyr Asp Gln Val Lys Glu Gln Asn Asp Asp Ile Glu Ala Tyr Val
                405                 410                 415

caa cta aaa ggc gat gct ggt tac ctc caa gga atc tac cgt acc ttg     1296
Gln Leu Lys Gly Asp Ala Gly Tyr Leu Gln Gly Ile Tyr Arg Thr Leu
            420                 425                 430

aaa gcc ata ttt ttc aat gaa ttc aga agg aat tcc aat ttg tat ttg     1344
Lys Ala Ile Phe Phe Asn Glu Phe Arg Arg Asn Ser Asn Leu Tyr Leu
        435                 440                 445

tac agg tta tca gac gat acg tat agt gta tat aaa agt tat atc ttg     1392
Tyr Arg Leu Ser Asp Asp Thr Tyr Ser Val Tyr Lys Ser Tyr Ile Leu
    450                 455                 460

ccc tat cga tgg ggt tcc ttg cca gga gtt agt cat ggt gat gat tta     1440
Pro Tyr Arg Trp Gly Ser Leu Pro Gly Val Ser His Gly Asp Asp Leu
465                 470                 475                 480

gga tat ctt ttt gca aac tcg ttg gat gtt cct att ttg gga aca acg     1488
Gly Tyr Leu Phe Ala Asn Ser Leu Asp Val Pro Ile Leu Gly Thr Thr
                485                 490                 495

cac att tct ata ccg caa gat gct atg cag act ctg gaa agg atg gtc     1536
His Ile Ser Ile Pro Gln Asp Ala Met Gln Thr Leu Glu Arg Met Val
            500                 505                 510

agg atc tgg acc aat ttt gta aag aat gga aaa cct aca tca aac act     1584
Arg Ile Trp Thr Asn Phe Val Lys Asn Gly Lys Pro Thr Ser Asn Thr
        515                 520                 525

gaa gat gca tca tgt gat aca aaa aga cat tta aac gac att ttt tgg     1632
Glu Asp Ala Ser Cys Asp Thr Lys Arg His Leu Asn Asp Ile Phe Trp
    530                 535                 540

gaa cca tac aac gac gaa gaa cca aaa tat ttg gac atg gga aaa gaa     1680
Glu Pro Tyr Asn Asp Glu Glu Pro Lys Tyr Leu Asp Met Gly Lys Glu
545                 550                 555                 560

aat ttt gaa atg aaa aat att ttg gaa cta aaa cgc atg atg ctt tgg     1728
Asn Phe Glu Met Lys Asn Ile Leu Glu Leu Lys Arg Met Met Leu Trp
                565                 570                 575

gat gaa gtt tat aga aat gcg aat ttg cgg ttt aga gtc tgt aat gaa     1776
Asp Glu Val Tyr Arg Asn Ala Asn Leu Arg Phe Arg Val Cys Asn Glu
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gaa agt att aga                                                   1788
Glu Ser Ile Arg
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gtccaaatat tttggttctt cgtcgttgta tggttcccaa aaaatgtcgt ttaaatgtct 180

ttttgtatca catgatgcat cttcagtgtt tgatgtaggt tttccattct ttacaaaatt 240

ggtccagatc ctgaccatcc tttccagagt ctgcatagca tcttgcggta tagaaatgtg 300

cgttgttccc aaaataggaa catccaacga gtttgcaaaa agatatccta aatcatcacc 360

atgactaact cctggcaagg aaccccatcg atagggcaag atataacttt tatatacact 420

atacgtatcg tctgataacc tgtacaaata caaattggaa ttccttctga attcattgaa 480

aaatatggct ttcaaggtac ggtagattcc ttggaggtaa ccagcatcgc cttttagttg 540

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cgagttgtcc atcatcagaa aatggacact tgctgctcca gcagattctc cagcaattgt 1140

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tcccaaagtt cgagcctgta cgaatcctgt ttttggattt gatattggtt ttggagactg 1560

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Met Leu Pro His Ser Ala
1 5

tta gtt tta ttt tta ttt ttt tta ttt ttc tta ttt aca cct gtc ttg 164
Leu Val Leu Phe Leu Phe Phe Leu Phe Phe Leu Phe Thr Pro Val Leu
10 15 20

tgc ata cta tgg gat aac cta gat cag cat ttg tgc aga gtt caa ttt 212
Cys Ile Leu Trp Asp Asn Leu Asp Gln His Leu Cys Arg Val Gln Phe
25 30 35

aac ggg atc acg gaa gga aaa ccg ttc cga tat aaa gat cat aaa aat 260
Asn Gly Ile Thr Glu Gly Lys Pro Phe Arg Tyr Lys Asp His Lys Asn
40 45 50

gat gta tat tgt tcc tat ttg gga att cct tat gca gaa ccg cct att 308
Asp Val Tyr Cys Ser Tyr Leu Gly Ile Pro Tyr Ala Glu Pro Pro Ile
55 60 65 70

gga cca ttg cga ttt cag tct cca aaa cca ata tca aat cca aaa aca 356
Gly Pro Leu Arg Phe Gln Ser Pro Lys Pro Ile Ser Asn Pro Lys Thr
75 80 85

gga ttc gtt cag gct cgg tct tta gga gac aaa tgt ttc cag gaa agt 404
Gly Phe Val Gln Ala Arg Ser Leu Gly Asp Lys Cys Phe Gln Glu Ser
90 95 100

cta ata tat tct tat gca gga agc gaa gat tgc tta tat ctg aat ata 452
Leu Ile Tyr Ser Tyr Ala Gly Ser Glu Asp Cys Leu Tyr Leu Asn Ile
105 110 115

ttc acg cca gag act gtt aat tct gcg aac aat aca aaa tat cct gta 500
Phe Thr Pro Glu Thr Val Asn Ser Ala Asn Asn Thr Lys Tyr Pro Val
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135 140 145 150

aat ttt ttt gga cct gat tat ttg atc agg gaa gga att att ttg gtc 596
Asn Phe Phe Gly Pro Asp Tyr Leu Ile Arg Glu Gly Ile Ile Leu Val
155 160 165

act atc aac tat aga tta gga gtt ttc ggt ttt cta tca gcg ccg gaa 644
Thr Ile Asn Tyr Arg Leu Gly Val Phe Gly Phe Leu Ser Ala Pro Glu

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Trp Asp Ile His Gly Asn Met Gly Leu Lys Asp Gln Arg Leu Ala Leu
        185                 190                 195

aaa tgg gtt tat gac aac atc gaa aaa ttt ggt gga gac aga gat aaa      740
Lys Trp Val Tyr Asp Asn Ile Glu Lys Phe Gly Gly Asp Arg Asp Lys
    200                 205                 210

atc act ata gct gga gaa tct gct gga gca gca agt gtt cat ttt ctg      788
Ile Thr Ile Ala Gly Glu Ser Ala Gly Ala Ala Ser Val His Phe Leu
215                 220                 225                 230

atg atg gac aat tct act aga aaa tac tac caa agg gca att ttg cag      836
Met Met Asp Asn Ser Thr Arg Lys Tyr Tyr Gln Arg Ala Ile Leu Gln
                235                 240                 245

agt ggg aca tta ctc aat ccg act gct aat caa att caa cct ctg cat      884
Ser Gly Thr Leu Leu Asn Pro Thr Ala Asn Gln Ile Gln Pro Leu His
            250                 255                 260

aga ttt gaa aaa cta aaa caa gtg ctg aac atc acg caa aaa caa gaa      932
Arg Phe Glu Lys Leu Lys Gln Val Leu Asn Ile Thr Gln Lys Gln Glu
        265                 270                 275

ctc cta aat ctg gac aaa aat caa att ttg cga gca gcc tta aac aga      980
Leu Leu Asn Leu Asp Lys Asn Gln Ile Leu Arg Ala Ala Leu Asn Arg
    280                 285                 290

gtc cca gat aac aac gac cac gaa agg gac aca gta cca gta ttt aat     1028
Val Pro Asp Asn Asn Asp His Glu Arg Asp Thr Val Pro Val Phe Asn
295                 300                 305                 310

cca gtc cta gaa tca cca gaa tct cca gac cca ata aca ttt cca tct     1076
Pro Val Leu Glu Ser Pro Glu Ser Pro Asp Pro Ile Thr Phe Pro Ser
                315                 320                 325

gct tta gaa aga atg aga aat ggt gaa ttt cct gac gtt gat gtc atc     1124
Ala Leu Glu Arg Met Arg Asn Gly Glu Phe Pro Asp Val Asp Val Ile
            330                 335                 340

att gga ttc aat agt gct gaa ggt tta aga tct atg cca aga gta acc     1172
Ile Gly Phe Asn Ser Ala Glu Gly Leu Arg Ser Met Pro Arg Val Thr
        345                 350                 355

aga gga aac atg gaa gtt tac aag act ttg aca aat ata gag aga gct     1220
Arg Gly Asn Met Glu Val Tyr Lys Thr Leu Thr Asn Ile Glu Arg Ala
    360                 365                 370

ata cct aga gat gct aat att tgg aaa aat cct aat ggc att gag gag     1268
Ile Pro Arg Asp Ala Asn Ile Trp Lys Asn Pro Asn Gly Ile Glu Glu
375                 380                 385                 390

aaa aaa ctt ata aaa atg ctt aca gag ttt tat gac caa gtt aaa gaa     1316
Lys Lys Leu Ile Lys Met Leu Thr Glu Phe Tyr Asp Gln Val Lys Glu
                395                 400                 405

caa aac gat gac atc gaa gcc tat gtc caa cta aaa ggc gat gct ggt     1364
Gln Asn Asp Asp Ile Glu Ala Tyr Val Gln Leu Lys Gly Asp Ala Gly
            410                 415                 420

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Tyr Leu Gln Gly Ile Tyr Arg Thr Leu Lys Ala Ile Phe Phe Asn Glu
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atc aaa aga aat tcc aac ttg tat ttg tat agg tta tca gat gat acg      1460
Ile Lys Arg Asn Ser Asn Leu Tyr Leu Tyr Arg Leu Ser Asp Asp Thr
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tat agt gta tat aaa agt tat atc ttg ccc tat cga tgg ggt tcc ttg      1508
Tyr Ser Val Tyr Lys Ser Tyr Ile Leu Pro Tyr Arg Trp Gly Ser Leu
455                 460                 465                 470

cca gga gtt agt cat ggt gat gat tta gga tat ctt ttt gca aac tct      1556
Pro Gly Val Ser His Gly Asp Asp Leu Gly Tyr Leu Phe Ala Asn Ser
                475                 480                 485

ttg gat gtt cct att ttg gga aca acg cac att tct ata ccg caa gat      1604
Leu Asp Val Pro Ile Leu Gly Thr Thr His Ile Ser Ile Pro Gln Asp
        490                 495                 500

gct atg cag act ctg gaa agg atg gtc agg atc tgg acc aat ttt gta      1652
Ala Met Gln Thr Leu Glu Arg Met Val Arg Ile Trp Thr Asn Phe Val
    505                 510                 515

aag aat gga aaa cct aca tca aac act gaa gat gca tca tgt gat aca      1700
Lys Asn Gly Lys Pro Thr Ser Asn Thr Glu Asp Ala Ser Cys Asp Thr
520                 525                 530

aaa aga cat tta aac gac att ttt tgg gaa cca tac aac gac gaa gaa      1748
Lys Arg His Leu Asn Asp Ile Phe Trp Glu Pro Tyr Asn Asp Glu Glu
535                 540                 545                 550

cca aaa tat ttg gac atg gga aaa gaa cat ttt gaa atg aaa aat att      1796
Pro Lys Tyr Leu Asp Met Gly Lys Glu His Phe Glu Met Lys Asn Ile
                555                 560                 565

ttg gaa cta aaa cgc atg atg ctt tgg gat gaa gtt tat aga aat gcg      1844
Leu Glu Leu Lys Arg Met Met Leu Trp Asp Glu Val Tyr Arg Asn Ala
            570                 575                 580

aat ttg cgg ttt aga gtc tgt aat gaa gaa agt att aga tga              1886
Asn Leu Arg Phe Arg Val Cys Asn Glu Glu Ser Ile Arg
        585                 590                 595

gttttttaa ttttacatac agccgagagg aaacatgact aaaattggaa agaaaaatca    1946

gaaaaagaaa aatcacatgg accatagtaa ctttattaca tgatttagtt tcaagtgtat    2006

caagaaaact tattgcatca aagaaaatat tattttgcca aaattcttgg aaaaacactt    2066

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cattaaatta gagttaatgt tgtaaattaa actatttttt atctatcaca accgcttaat    2546
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20 25 30

Leu Cys Arg Val Gln Phe Asn Gly Ile Thr Glu Gly Lys Pro Phe Arg
35 40 45

Tyr Lys Asp His Lys Asn Asp Val Tyr Cys Ser Tyr Leu Gly Ile Pro
50 55 60

Tyr Ala Glu Pro Pro Ile Gly Pro Leu Arg Phe Gln Ser Pro Lys Pro
65 70 75 80

Ile Ser Asn Pro Lys Thr Gly Phe Val Gln Ala Arg Ser Leu Gly Asp
85 90 95

Lys Cys Phe Gln Glu Ser Leu Ile Tyr Ser Tyr Ala Gly Ser Glu Asp
100 105 110

Cys Leu Tyr Leu Asn Ile Phe Thr Pro Glu Thr Val Asn Ser Ala Asn
115 120 125

Asn Thr Lys Tyr Pro Val Met Phe Trp Ile His Gly Gly Ala Phe Asn
130 135 140

Gln Gly Ser Gly Ser Tyr Asn Phe Phe Gly Pro Asp Tyr Leu Ile Arg
145 150 155 160

Glu Gly Ile Ile Leu Val Thr Ile Asn Tyr Arg Leu Gly Val Phe Gly
165 170 175

Phe Leu Ser Ala Pro Glu Trp Asp Ile His Gly Asn Met Gly Leu Lys
180 185 190

Asp Gln Arg Leu Ala Leu Lys Trp Val Tyr Asp Asn Ile Glu Lys Phe
195 200 205

Gly Gly Asp Arg Asp Lys Ile Thr Ile Ala Gly Glu Ser Ala Gly Ala
210 215 220

Ala Ser Val His Phe Leu Met Met Asp Asn Ser Thr Arg Lys Tyr Tyr
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Gln Arg Ala Ile Leu Gln Ser Gly Thr Leu Leu Asn Pro Thr Ala Asn
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Gln Ile Gln Pro Leu His Arg Phe Glu Lys Leu Lys Gln Val Leu Asn
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Ile Thr Gln Lys Gln Glu Leu Leu Asn Leu Asp Lys Asn Gln Ile Leu
275 280 285

Arg Ala Ala Leu Asn Arg Val Pro Asp Asn Asn Asp His Glu Arg Asp
290 295 300

Thr Val Pro Val Phe Asn Pro Val Leu Glu Ser Pro Glu Ser Pro Asp
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Pro Ile Thr Phe Pro Ser Ala Leu Glu Arg Met Arg Asn Gly Glu Phe
325 330 335

Pro Asp Val Asp Val Ile Ile Gly Phe Asn Ser Ala Glu Gly Leu Arg
340 345 350

Ser Met Pro Arg Val Thr Arg Gly Asn Met Glu Val Tyr Lys Thr Leu
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Thr Asn Ile Glu Arg Ala Ile Pro Arg Asp Ala Asn Ile Trp Lys Asn
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Pro Asn Gly Ile Glu Glu Lys Lys Leu Ile Lys Met Leu Thr Glu Phe
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Leu Lys Gly Asp Ala Gly Tyr Leu Gln Gly Ile Tyr Arg Thr Leu Lys
420 425 430

Ala Ile Phe Phe Asn Glu Ile Lys Arg Asn Ser Asn Leu Tyr Leu Tyr
435 440 445

Arg Leu Ser Asp Asp Thr Tyr Ser Val Tyr Lys Ser Tyr Ile Leu Pro
450 455 460

Tyr Arg Trp Gly Ser Leu Pro Gly Val Ser His Gly Asp Asp Leu Gly
465 470 475 480

Tyr Leu Phe Ala Asn Ser Leu Asp Val Pro Ile Leu Gly Thr Thr His
485 490 495

Ile Ser Ile Pro Gln Asp Ala Met Gln Thr Leu Glu Arg Met Val Arg
500 505 510

Ile Trp Thr Asn Phe Val Lys Asn Gly Lys Pro Thr Ser Asn Thr Glu
515 520 525

Asp Ala Ser Cys Asp Thr Lys Arg His Leu Asn Asp Ile Phe Trp Glu
530 535 540

Pro Tyr Asn Asp Glu Glu Pro Lys Tyr Leu Asp Met Gly Lys Glu His
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Phe Glu Met Lys Asn Ile Leu Glu Leu Lys Arg Met Met Leu Trp Asp
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Ser Ile Arg
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cagaggttga atttgattag cagtcggatt gagtaatgtc ccactctgca aaattgccct 1980

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agattctcca gctatagtga ttttatctct gtctccacca aatttttcga tgttgtcata 2100

aacccatttt agtgccaatc tctggtcttt tagacccata tttccatgga tatcccattc 2160

cggcgctgat agaaaaccga aaactcctaa tctatagttg atagtgacca aaataattcc 2220

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tggcgtgaat atattcagat ataagcaatc ttcgcttcct gcataagaat atattagact 2400

ttcctggaaa catttgtctc ctaaagaccg agcctgaacg aatcctgttt ttggatttga 2460

tattggtttt ggagactgaa atcgcaatgg tccaataggc ggttctgcat aaggaattcc 2520

caaataggaa caatatacat cattttatg atctttatat cggaacggtt ttccttccgt 2580

gatcccgtta aattgaactc tgcacaaatg ctgatctagg ttatcccata gtatgcacaa 2640

gacaggtgta aataagaaaa ataaaaaaaa taaaaataaa actaatgcac tgtgaggtaa 2700

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1               5                  10                  15

acg gaa gga aaa ccg ttc cga tat aaa gat cat aaa aat gat gta tat       96
Thr Glu Gly Lys Pro Phe Arg Tyr Lys Asp His Lys Asn Asp Val Tyr
            20                  25                  30

tgt tcc tat ttg gga att cct tat gca gaa ccg cct att gga cca ttg      144
Cys Ser Tyr Leu Gly Ile Pro Tyr Ala Glu Pro Pro Ile Gly Pro Leu
        35                  40                  45

cga ttt cag tct cca aaa cca ata tca aat cca aaa aca gga ttc gtt      192
Arg Phe Gln Ser Pro Lys Pro Ile Ser Asn Pro Lys Thr Gly Phe Val
    50                  55                  60

cag gct cgg tct tta gga gac aaa tgt ttc cag gaa agt cta ata tat      240
Gln Ala Arg Ser Leu Gly Asp Lys Cys Phe Gln Glu Ser Leu Ile Tyr
65                  70                  75                  80

tct tat gca gga agc gaa gat tgc tta tat ctg aat ata ttc acg cca      288
Ser Tyr Ala Gly Ser Glu Asp Cys Leu Tyr Leu Asn Ile Phe Thr Pro
                85                  90                  95

gag act gtt aat tct gcg aac aat aca aaa tat cct gta atg ttc tgg      336
Glu Thr Val Asn Ser Ala Asn Asn Thr Lys Tyr Pro Val Met Phe Trp
            100                 105                 110

atc cat gga ggc gca ttc aac caa gga tca gga tct tat aat ttt ttt      384
Ile His Gly Gly Ala Phe Asn Gln Gly Ser Gly Ser Tyr Asn Phe Phe
        115                 120                 125
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gga cct gat tat ttg atc agg gaa gga att att ttg gtc act atc aac      432
Gly Pro Asp Tyr Leu Ile Arg Glu Gly Ile Ile Leu Val Thr Ile Asn
    130                 135                 140

tat aga tta gga gtt ttc ggt ttt cta tca gcg ccg gaa tgg gat atc      480
Tyr Arg Leu Gly Val Phe Gly Phe Leu Ser Ala Pro Glu Trp Asp Ile
145                 150                 155                 160

cat gga aat atg ggt cta aaa gac cag aga ttg gca cta aaa tgg gtt      528
His Gly Asn Met Gly Leu Lys Asp Gln Arg Leu Ala Leu Lys Trp Val
                165                 170                 175

tat gac aac atc gaa aaa ttt ggt gga gac aga gat aaa atc act ata      576
Tyr Asp Asn Ile Glu Lys Phe Gly Gly Asp Arg Asp Lys Ile Thr Ile
            180                 185                 190

gct gga gaa tct gct gga gca gca agt gtt cat ttt ctg atg atg gac      624
Ala Gly Glu Ser Ala Gly Ala Ala Ser Val His Phe Leu Met Met Asp
        195                 200                 205

aat tct act aga aaa tac tac caa agg gca att ttg cag agt ggg aca      672
Asn Ser Thr Arg Lys Tyr Tyr Gln Arg Ala Ile Leu Gln Ser Gly Thr
    210                 215                 220

tta ctc aat ccg act gct aat caa att caa cct ctg cat aga ttt gaa      720
Leu Leu Asn Pro Thr Ala Asn Gln Ile Gln Pro Leu His Arg Phe Glu
225                 230                 235                 240

aaa cta aaa caa gtg ctg aac atc acg caa aaa caa gaa ctc cta aat      768
Lys Leu Lys Gln Val Leu Asn Ile Thr Gln Lys Gln Glu Leu Leu Asn
                245                 250                 255

ctg gac aaa aat caa att ttg cga gca gcc tta aac aga gtc cca gat      816
Leu Asp Lys Asn Gln Ile Leu Arg Ala Ala Leu Asn Arg Val Pro Asp
            260                 265                 270

aac aac gac cac gaa agg gac aca gta cca gta ttt aat cca gtc cta      864
Asn Asn Asp His Glu Arg Asp Thr Val Pro Val Phe Asn Pro Val Leu
        275                 280                 285

gaa tca cca gaa tct cca gac cca ata aca ttt cca tct gct tta gaa      912
Glu Ser Pro Glu Ser Pro Asp Pro Ile Thr Phe Pro Ser Ala Leu Glu
    290                 295                 300

aga atg aga aat ggt gaa ttt cct gac gtt gat gtc atc att gga ttc      960
Arg Met Arg Asn Gly Glu Phe Pro Asp Val Asp Val Ile Ile Gly Phe
305                 310                 315                 320

aat agt gct gaa ggt tta aga tct atg cca aga gta acc aga gga aac     1008
Asn Ser Ala Glu Gly Leu Arg Ser Met Pro Arg Val Thr Arg Gly Asn
                325                 330                 335

atg gaa gtt tac aag act ttg aca aat ata gag aga gct ata cct aga     1056
Met Glu Val Tyr Lys Thr Leu Thr Asn Ile Glu Arg Ala Ile Pro Arg
            340                 345                 350

gat gct aat att tgg aaa aat cct aat ggc att gag gag aaa aaa ctt     1104
Asp Ala Asn Ile Trp Lys Asn Pro Asn Gly Ile Glu Glu Lys Lys Leu
        355                 360                 365

ata aaa atg ctt aca gag ttt tat gac caa gtt aaa gaa caa aac gat     1152
Ile Lys Met Leu Thr Glu Phe Tyr Asp Gln Val Lys Glu Gln Asn Asp
    370                 375                 380
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gac atc gaa gcc tat gtc caa cta aaa ggc gat gct ggt tat ctc caa      1200
Asp Ile Glu Ala Tyr Val Gln Leu Lys Gly Asp Ala Gly Tyr Leu Gln
385                 390                 395                 400

gga att tac cgt acc ttg aaa gcc ata ttt ttc aat gaa atc aaa aga      1248
Gly Ile Tyr Arg Thr Leu Lys Ala Ile Phe Phe Asn Glu Ile Lys Arg
                405                 410                 415

aat tcc aac ttg tat ttg tat agg tta tca gat gat acg tat agt gta      1296
Asn Ser Asn Leu Tyr Leu Tyr Arg Leu Ser Asp Asp Thr Tyr Ser Val
            420                 425                 430

tat aaa agt tat atc ttg ccc tat cga tgg ggt tcc ttg cca gga gtt      1344
Tyr Lys Ser Tyr Ile Leu Pro Tyr Arg Trp Gly Ser Leu Pro Gly Val
        435                 440                 445

agt cat ggt gat gat tta gga tat ctt ttt gca aac tct ttg gat gtt      1392
Ser His Gly Asp Asp Leu Gly Tyr Leu Phe Ala Asn Ser Leu Asp Val
    450                 455                 460

cct att ttg gga aca acg cac att tct ata ccg caa gat gct atg cag      1440
Pro Ile Leu Gly Thr Thr His Ile Ser Ile Pro Gln Asp Ala Met Gln
465                 470                 475                 480

act ctg gaa agg atg gtc agg atc tgg acc aat ttt gta aag aat gga      1488
Thr Leu Glu Arg Met Val Arg Ile Trp Thr Asn Phe Val Lys Asn Gly
                485                 490                 495

aaa cct aca tca aac act gaa gat gca tca tgt gat aca aaa aga cat      1536
Lys Pro Thr Ser Asn Thr Glu Asp Ala Ser Cys Asp Thr Lys Arg His
            500                 505                 510

tta aac gac att ttt tgg gaa cca tac aac gac gaa gaa cca aaa tat      1584
Leu Asn Asp Ile Phe Trp Glu Pro Tyr Asn Asp Glu Glu Pro Lys Tyr
        515                 520                 525

ttg gac atg gga aaa gaa cat ttt gaa atg aaa aat att ttg gaa cta      1632
Leu Asp Met Gly Lys Glu His Phe Glu Met Lys Asn Ile Leu Glu Leu
    530                 535                 540

aaa cgc atg atg ctt tgg gat gaa gtt tat aga aat gcg aat ttg cgg      1680
Lys Arg Met Met Leu Trp Asp Glu Val Tyr Arg Asn Ala Asn Leu Arg
545                 550                 555                 560

ttt aga gtc tgt aat gaa gaa agt att aga                             1710
Phe Arg Val Cys Asn Glu Glu Ser Ile Arg
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<220>
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1               5                   10                  15

tta ttt aca cct gtc ttg tgc ata cta tgg gat aac cta gat cag cat      96
Leu Phe Thr Pro Val Leu Cys Ile Leu Trp Asp Asn Leu Asp Gln His
            20                  25                  30

ttg tgc aga gtt caa ttt aac ggg atc acg gaa gga aaa ccg ttc cga     144
Leu Cys Arg Val Gln Phe Asn Gly Ile Thr Glu Gly Lys Pro Phe Arg
        35                  40                  45

tat aaa gat cat aaa aat gat gta tat tgt tcc tat ttg gga att cct     192
Tyr Lys Asp His Lys Asn Asp Val Tyr Cys Ser Tyr Leu Gly Ile Pro
    50                  55                  60

tat gca gaa ccg cct att gga cca ttg cga ttt cag tct cca aaa cca     240
Tyr Ala Glu Pro Pro Ile Gly Pro Leu Arg Phe Gln Ser Pro Lys Pro
65                  70                  75                  80

ata tca aat cca aaa aca gga ttc gtt cag gct cgg tct tta gga gac     288
Ile Ser Asn Pro Lys Thr Gly Phe Val Gln Ala Arg Ser Leu Gly Asp
                85                  90                  95

aaa tgt ttc cag gaa agt cta ata tat tct tat gca gga agc gaa gat     336
Lys Cys Phe Gln Glu Ser Leu Ile Tyr Ser Tyr Ala Gly Ser Glu Asp
            100                 105                 110

tgc tta tat ctg aat ata ttc acg cca gag act gtt aat tct gcg aac     384
Cys Leu Tyr Leu Asn Ile Phe Thr Pro Glu Thr Val Asn Ser Ala Asn
        115                 120                 125

aat aca aaa tat cct gta atg ttc tgg atc cat gga ggc gca ttc aac     432
Asn Thr Lys Tyr Pro Val Met Phe Trp Ile His Gly Gly Ala Phe Asn
    130                 135                 140

caa gga tca gga tct tat aat ttt ttt gga cct gat tat ttg atc agg     480
Gln Gly Ser Gly Ser Tyr Asn Phe Phe Gly Pro Asp Tyr Leu Ile Arg
145                 150                 155                 160

gaa gga att att ttg gtc act atc aac tat aga tta gga gtt ttc ggt     528
Glu Gly Ile Ile Leu Val Thr Ile Asn Tyr Arg Leu Gly Val Phe Gly
                165                 170                 175

ttt cta tca gcg ccg gaa tgg gat atc cat gga aat atg ggt cta aaa     576
Phe Leu Ser Ala Pro Glu Trp Asp Ile His Gly Asn Met Gly Leu Lys
            180                 185                 190

gac cag aga ttg gca cta aaa tgg gtt tat gac aac atc gaa aaa ttt     624
Asp Gln Arg Leu Ala Leu Lys Trp Val Tyr Asp Asn Ile Glu Lys Phe
        195                 200                 205

ggt gga gac aga gat aaa atc act ata gct gga gaa tct gct gga gca     672
Gly Gly Asp Arg Asp Lys Ile Thr Ile Ala Gly Glu Ser Ala Gly Ala
    210                 215                 220

gca agt gtt cat ttt ctg atg atg gac aat tct act aga aaa tac tac     720
Ala Ser Val His Phe Leu Met Met Asp Asn Ser Thr Arg Lys Tyr Tyr
225                 230                 235                 240

caa agg gca att ttg cag agt ggg aca tta ctc aat ccg act gct aat     768
Gln Arg Ala Ile Leu Gln Ser Gly Thr Leu Leu Asn Pro Thr Ala Asn
                245                 250                 255

caa att caa cct ctg cat aga ttt gaa aaa cta aaa caa gtg ctg aac     816
Gln Ile Gln Pro Leu His Arg Phe Glu Lys Leu Lys Gln Val Leu Asn
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            260                 265                 270

atc acg caa aaa caa gaa ctc cta aat ctg gac aaa aat caa att ttg      864
Ile Thr Gln Lys Gln Glu Leu Leu Asn Leu Asp Lys Asn Gln Ile Leu
        275                 280                 285

cga gca gcc tta aac aga gtc cca gat aac aac gac cac gaa agg gac      912
Arg Ala Ala Leu Asn Arg Val Pro Asp Asn Asn Asp His Glu Arg Asp
    290                 295                 300

aca gta cca gta ttt aat cca gtc cta gaa tca cca gaa tct cca gac      960
Thr Val Pro Val Phe Asn Pro Val Leu Glu Ser Pro Glu Ser Pro Asp
305                 310                 315                 320

cca ata aca ttt cca tct gct tta gaa aga atg aga aat ggt gaa ttt     1008
Pro Ile Thr Phe Pro Ser Ala Leu Glu Arg Met Arg Asn Gly Glu Phe
                325                 330                 335

cct gac gtt gat gtc atc att gga ttc aat agt gct gaa ggt tta aga     1056
Pro Asp Val Asp Val Ile Ile Gly Phe Asn Ser Ala Glu Gly Leu Arg
            340                 345                 350

tct atg cca aga gta acc aga gga aac atg gaa gtt tac aag act ttg     1104
Ser Met Pro Arg Val Thr Arg Gly Asn Met Glu Val Tyr Lys Thr Leu
        355                 360                 365

aca aat ata gag aga gct ata cct aga gat gct aat att tgg aaa aat     1152
Thr Asn Ile Glu Arg Ala Ile Pro Arg Asp Ala Asn Ile Trp Lys Asn
    370                 375                 380

cct aat ggc att gag gag aaa aaa ctt ata aaa atg ctt aca gag ttt     1200
Pro Asn Gly Ile Glu Glu Lys Lys Leu Ile Lys Met Leu Thr Glu Phe
385                 390                 395                 400

tat gac caa gtt aaa gaa caa aac gat gac atc gaa gcc tat gtc caa     1248
Tyr Asp Gln Val Lys Glu Gln Asn Asp Asp Ile Glu Ala Tyr Val Gln
                405                 410                 415

cta aaa ggc gat gct ggt tat ctc caa gga att tac cgt acc ttg aaa     1296
Leu Lys Gly Asp Ala Gly Tyr Leu Gln Gly Ile Tyr Arg Thr Leu Lys
            420                 425                 430

gcc ata ttt ttc aat gaa atc aaa aga aat tcc aac ttg tat ttg tat     1344
Ala Ile Phe Phe Asn Glu Ile Lys Arg Asn Ser Asn Leu Tyr Leu Tyr
        435                 440                 445

agg tta tca gat gat acg tat agt gta tat aaa agt tat atc ttg ccc     1392
Arg Leu Ser Asp Asp Thr Tyr Ser Val Tyr Lys Ser Tyr Ile Leu Pro
    450                 455                 460

tat cga tgg ggt tcc ttg cca gga gtt agt cat ggt gat gat tta gga     1440
Tyr Arg Trp Gly Ser Leu Pro Gly Val Ser His Gly Asp Asp Leu Gly
465                 470                 475                 480

tat ctt ttt gca aac tct ttg gat gtt cct att ttg gga aca acg cac     1488
Tyr Leu Phe Ala Asn Ser Leu Asp Val Pro Ile Leu Gly Thr Thr His
                485                 490                 495

att tct ata ccg caa gat gct atg cag act ctg gaa agg atg gtc agg     1536
Ile Ser Ile Pro Gln Asp Ala Met Gln Thr Leu Glu Arg Met Val Arg
            500                 505                 510

atc tgg acc aat ttt gta aag aat gga aaa cct aca tca aac act gaa     1584
Ile Trp Thr Asn Phe Val Lys Asn Gly Lys Pro Thr Ser Asn Thr Glu
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        515                 520                 525

gat gca tca tgt gat aca aaa aga cat tta aac gac att ttt tgg gaa     1632
Asp Ala Ser Cys Asp Thr Lys Arg His Leu Asn Asp Ile Phe Trp Glu
    530                 535                 540

cca tac aac gac gaa gaa cca aaa tat ttg gac atg gga aaa gaa cat     1680
Pro Tyr Asn Asp Glu Glu Pro Lys Tyr Leu Asp Met Gly Lys Glu His
545                 550                 555                 560

ttt gaa atg aaa aat att ttg gaa cta aaa cgc atg atg ctt tgg gat     1728
Phe Glu Met Lys Asn Ile Leu Glu Leu Lys Arg Met Met Leu Trp Asp
                565                 570                 575

gaa gtt tat aga aat gcg aat ttg cgg ttt aga gtc tgt aat gaa gaa     1776
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agt att aga                                                       1785
Ser Ile Arg
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gtccaaatat tttggttctt cgtcgttgta tggttcccaa aaaatgtcgt ttaaatgtct    180

ttttgtatca catgatgcat cttcagtgtt tgatgtaggt tttccattct ttacaaaatt    240

ggtccagatc ctgaccatcc tttccagagt ctgcatagca tcttgcggta tagaaatgtg    300

cgttgttccc aaaataggaa catccaaaga gtttgcaaaa agatatccta aatcatcacc    360

atgactaact cctggcaagg aaccccatcg atagggcaag atataacttt tatatacact    420

atacgtatca tctgataacc tatacaaata caagttggaa tttcttttga tttcattgaa    480

aaatatggct ttcaaggtac ggtaaattcc ttggagataa ccagcatcgc cttttagttg    540

gacataggct tcgatgtcat cgttttgttc tttaacttgg tcataaaact ctgtaagcat    600

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ttcaccattt ctcattcttt ctaaagcaga tggaaatgtt attgggtctg gagattctgg    840

tgattctagg actggattaa atactggtac tgtgtccctt tcgtggtcgt tgttatctgg    900

gactctgttt aaggctgctc gcaaaatttg atttttgtcc agatttagga gttcttgttt    960

ttgcgtgatg ttcagcactt gttttagttt ttcaaatcta tgcagaggtt gaatttgatt   1020

agcagtcgga ttgagtaatg tcccactctg caaaattgcc ctttggtagt attttctagt   1080
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agaattgtcc atcatcagaa aatgaacact tgctgctcca gcagattctc cagctatagt 1140

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tctctggtct tttagaccca tatttccatg gatatcccat tccggcgctg atagaaaacc 1260

gaaaactcct aatctatagt tgatagtgac caaaataatt ccttccctga tcaaataatc 1320

aggtccaaaa aaattataag atcctgatcc ttggttgaat gcgcctccat ggatccagaa 1380

cattacagga tattttgtat tgttcgcaga attaacagtc tctggcgtga atatattcag 1440

atataagcaa tcttcgcttc ctgcataaga atatattaga ctttcctgga aacatttgtc 1500

tcctaaagac cgagcctgaa cgaatcctgt ttttggattt gatattggtt ttggagactg 1560

aaatcgcaat ggtccaatag gcggttctgc ataaggaatt cccaaatagg aacaatatac 1620

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aaa gga aaa gag caa att agt gaa aaa gga aat gtg ttc cat agt tat 97
Lys Gly Lys Glu Gln Ile Ser Glu Lys Gly Asn Val Phe His Ser Tyr
15 20 25

tct gga att cca tat gcc aaa cct cct gta ggt gat cta aga ttt aag 145
Ser Gly Ile Pro Tyr Ala Lys Pro Pro Val Gly Asp Leu Arg Phe Lys
30 35 40 45

cca cct caa cct gca gaa cct tgg tca ggt gtt ctt gat gct agt aaa 193
Pro Pro Gln Pro Ala Glu Pro Trp Ser Gly Val Leu Asp Ala Ser Lys
50 55 60

gaa ggg aat agt tgt aga tca gta cat ttt att aaa aaa att aaa gta 241
Glu Gly Asn Ser Cys Arg Ser Val His Phe Ile Lys Lys Ile Lys Val
65 70 75

ggg gct gaa gat tgt tta tac ctc aat gtc tat gta cca aaa aca tca 289
Gly Ala Glu Asp Cys Leu Tyr Leu Asn Val Tyr Val Pro Lys Thr Ser
80 85 90

gag aaa tca ctt ctt cca gta atg gta tgg ata cat gga gga ggc ttc 337
Glu Lys Ser Leu Leu Pro Val Met Val Trp Ile His Gly Gly Gly Phe

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    95                  100                 105

ttc atg gga tct gga aat agt gat atg tat ggt cct gaa tat ttg atg      385
Phe Met Gly Ser Gly Asn Ser Asp Met Tyr Gly Pro Glu Tyr Leu Met
110                 115                 120                 125

gat tat gga att gtt ctg gtt act ttc aat tat cga tta ggt gtt ttg      433
Asp Tyr Gly Ile Val Leu Val Thr Phe Asn Tyr Arg Leu Gly Val Leu
                130                 135                 140

gga ttt ttg aac ctg gga ata gaa gaa gcg cct ggc aat gtt ggt ttg      481
Gly Phe Leu Asn Leu Gly Ile Glu Glu Ala Pro Gly Asn Val Gly Leu
            145                 150                 155

atg gac cag gtt gaa gct cta aaa tgg gta aaa aac aat att gca tcc      529
Met Asp Gln Val Glu Ala Leu Lys Trp Val Lys Asn Asn Ile Ala Ser
        160                 165                 170

ttt ggt ggt gac ccc aac aat gtg act att ttt gga gaa tca gca ggt      577
Phe Gly Gly Asp Pro Asn Asn Val Thr Ile Phe Gly Glu Ser Ala Gly
    175                 180                 185

ggt gca agt gtt cat tat ttg atg tta tca gat ctt tcc aaa gga ctt      625
Gly Ala Ser Val His Tyr Leu Met Leu Ser Asp Leu Ser Lys Gly Leu
190                 195                 200                 205

ttt cat aaa gcg atc tca caa agt gga agt gct ttt aat cct tgg gca      673
Phe His Lys Ala Ile Ser Gln Ser Gly Ser Ala Phe Asn Pro Trp Ala
                210                 215                 220

ctt caa cat gat aat aat aaa gaa aat gca ttc cgc ctc tgc aaa ctt      721
Leu Gln His Asp Asn Asn Lys Glu Asn Ala Phe Arg Leu Cys Lys Leu
            225                 230                 235

ctg ggt cat cct gtc gat aac gag aca gaa gct cta aaa atc ctt cgt      769
Leu Gly His Pro Val Asp Asn Glu Thr Glu Ala Leu Lys Ile Leu Arg
        240                 245                 250

caa gcc ccc ata gat gat ctt ata gac aac aga ata aaa cca aaa gac      817
Gln Ala Pro Ile Asp Asp Leu Ile Asp Asn Arg Ile Lys Pro Lys Asp
    255                 260                 265

aaa ggc caa ctt att ata gac tat cct ttt cta cca aca ata gaa aaa      865
Lys Gly Gln Leu Ile Ile Asp Tyr Pro Phe Leu Pro Thr Ile Glu Lys
270                 275                 280                 285

cgt tat caa aat ttt gaa cca ttc ttg gac cag tct cca tta tca aaa      913
Arg Tyr Gln Asn Phe Glu Pro Phe Leu Asp Gln Ser Pro Leu Ser Lys
                290                 295                 300

atg caa tca ggc aat ttc aca aaa gtc cca ttt ata tgt gga tac aac      961
Met Gln Ser Gly Asn Phe Thr Lys Val Pro Phe Ile Cys Gly Tyr Asn
            305                 310                 315

agt gct gaa gga att tta ggt tta atg gac ttc aag gat gac cca aat     1009
Ser Ala Glu Gly Ile Leu Gly Leu Met Asp Phe Lys Asp Asp Pro Asn
        320                 325                 330

ata ttt gag aag ttt gaa gct gat ttt gaa aga ttt gta cca gta gat     1057
Ile Phe Glu Lys Phe Glu Ala Asp Phe Glu Arg Phe Val Pro Val Asp
    335                 340                 345

ttg aat cta act tta agg tct aag gaa tct aaa aaa ttg gct gaa gaa     1105
Leu Asn Leu Thr Leu Arg Ser Lys Glu Ser Lys Lys Leu Ala Glu Glu
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350                 355                 360                 365

atg aga aag ttt tat tac caa gac gaa cct gtt tct tca gac aac aaa     1153
Met Arg Lys Phe Tyr Tyr Gln Asp Glu Pro Val Ser Ser Asp Asn Lys
                370                 375                 380

gaa aaa ttt gtc agt gtt att agt gat act tgg ttt ttg aga ggg att     1201
Glu Lys Phe Val Ser Val Ile Ser Asp Thr Trp Phe Leu Arg Gly Ile
            385                 390                 395

aaa aat act gca aga tat ata att gaa cat tcc tca gaa ccg tta tat     1249
Lys Asn Thr Ala Arg Tyr Ile Ile Glu His Ser Ser Glu Pro Leu Tyr
        400                 405                 410

tta tat gtt tat agt ttt gat gat ttt ggt ttt ttg aag aaa ctt gta     1297
Leu Tyr Val Tyr Ser Phe Asp Asp Phe Gly Phe Leu Lys Lys Leu Val
    415                 420                 425

tta gat cct aat att gaa gga gca gct cat gga gat gag ctg gga tat     1345
Leu Asp Pro Asn Ile Glu Gly Ala Ala His Gly Asp Glu Leu Gly Tyr
430                 435                 440                 445

ctt ttc aag atg agt ttt aca gaa ttt cca aaa gat tta cca agt gca     1393
Leu Phe Lys Met Ser Phe Thr Glu Phe Pro Lys Asp Leu Pro Ser Ala
                450                 455                 460

gtg gtg aat agg gaa cga ttg ttg caa ctt tgg aca aat ttt gca aaa     1441
Val Val Asn Arg Glu Arg Leu Leu Gln Leu Trp Thr Asn Phe Ala Lys
            465                 470                 475

aca gga aat ccc act cct gaa atc aat gat gtt ata aca aca aaa tgg     1489
Thr Gly Asn Pro Thr Pro Glu Ile Asn Asp Val Ile Thr Thr Lys Trp
        480                 485                 490

gat aaa gct act gag gaa aaa tca gat cat atg gat atc gat aat act     1537
Asp Lys Ala Thr Glu Glu Lys Ser Asp His Met Asp Ile Asp Asn Thr
    495                 500                 505

ttg aga atg att cca gat cct gat gca aaa cga ctt aga ttt tgg aat     1585
Leu Arg Met Ile Pro Asp Pro Asp Ala Lys Arg Leu Arg Phe Trp Asn
510                 515                 520                 525

aaa ttt tta tgataaatat accaattatc gattttatta tagagtttct             1634
Lys Phe Leu

gtattagtat aattatcacg tttagatgta cgagattcaa ttggctctaa ttgaagtata   1694

tttcgatttc aaatttactc tgattattgg aaaaaaagct tttacagttg taataatcaa   1754

gaagtaggtg gtaaatttag aacaaattct gttttagtga tttgcgcatt caacagatgg   1814

tgtactgtgc ctaaatttgt cgctcttctt gaagaactga actaaaaatg tgattaatgg   1874

acgccacatt atttatattt gatattatta ccatctttgt atcatatttg cttttatttt   1934

ttcatttttt ttttatttca aatatattgt ttttttataa aaaaaaaaaa aaaaaaaaaa   1994

aaaaaaaaaa aaa                                                     2007
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<210> 37
<211> 528
<212> PRT

<213> Ctenocephalides felis

<400> 37

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Met Ala Asp Leu Gln Val Thr Leu Leu Gln Gly Thr Leu Lys Gly Lys
1               5                  10                  15

Glu Gln Ile Ser Glu Lys Gly Asn Val Phe His Ser Tyr Ser Gly Ile
            20                  25                  30

Pro Tyr Ala Lys Pro Pro Val Gly Asp Leu Arg Phe Lys Pro Pro Gln
        35                  40                  45

Pro Ala Glu Pro Trp Ser Gly Val Leu Asp Ala Ser Lys Glu Gly Asn
    50                  55                  60

Ser Cys Arg Ser Val His Phe Ile Lys Lys Ile Lys Val Gly Ala Glu
65                  70                  75                  80

Asp Cys Leu Tyr Leu Asn Val Tyr Val Pro Lys Thr Ser Glu Lys Ser
                85                  90                  95

Leu Leu Pro Val Met Val Trp Ile His Gly Gly Gly Phe Phe Met Gly
            100                 105                 110

Ser Gly Asn Ser Asp Met Tyr Gly Pro Glu Tyr Leu Met Asp Tyr Gly
        115                 120                 125

Ile Val Leu Val Thr Phe Asn Tyr Arg Leu Gly Val Leu Gly Phe Leu
    130                 135                 140

Asn Leu Gly Ile Glu Glu Ala Pro Gly Asn Val Gly Leu Met Asp Gln
145                 150                 155                 160

Val Glu Ala Leu Lys Trp Val Lys Asn Asn Ile Ala Ser Phe Gly Gly
                165                 170                 175

Asp Pro Asn Asn Val Thr Ile Phe Gly Glu Ser Ala Gly Gly Ala Ser
            180                 185                 190

Val His Tyr Leu Met Leu Ser Asp Leu Ser Lys Gly Leu Phe His Lys
        195                 200                 205

Ala Ile Ser Gln Ser Gly Ser Ala Phe Asn Pro Trp Ala Leu Gln His
    210                 215                 220

Asp Asn Asn Lys Glu Asn Ala Phe Arg Leu Cys Lys Leu Leu Gly His
225                 230                 235                 240
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Pro Val Asp Asn Glu Thr Glu Ala Leu Lys Ile Leu Arg Gln Ala Pro
                245                 250                 255

Ile Asp Asp Leu Ile Asp Asn Arg Ile Lys Pro Lys Asp Lys Gly Gln
            260                 265                 270

Leu Ile Ile Asp Tyr Pro Phe Leu Pro Thr Ile Glu Lys Arg Tyr Gln
        275                 280                 285

Asn Phe Glu Pro Phe Leu Asp Gln Ser Pro Leu Ser Lys Met Gln Ser
    290                 295                 300

Gly Asn Phe Thr Lys Val Pro Phe Ile Cys Gly Tyr Asn Ser Ala Glu
305                 310                 315                 320

Gly Ile Leu Gly Leu Met Asp Phe Lys Asp Asp Pro Asn Ile Phe Glu
                325                 330                 335

Lys Phe Glu Ala Asp Phe Glu Arg Phe Val Pro Val Asp Leu Asn Leu
            340                 345                 350

Thr Leu Arg Ser Lys Glu Ser Lys Lys Leu Ala Glu Glu Met Arg Lys
        355                 360                 365

Phe Tyr Tyr Gln Asp Glu Pro Val Ser Ser Asp Asn Lys Glu Lys Phe
    370                 375                 380

Val Ser Val Ile Ser Asp Thr Trp Phe Leu Arg Gly Ile Lys Asn Thr
385                 390                 395                 400

Ala Arg Tyr Ile Ile Glu His Ser Ser Glu Pro Leu Tyr Leu Tyr Val
                405                 410                 415

Tyr Ser Phe Asp Asp Phe Gly Phe Leu Lys Lys Leu Val Leu Asp Pro
            420                 425                 430

Asn Ile Glu Gly Ala Ala His Gly Asp Glu Leu Gly Tyr Leu Phe Lys
        435                 440                 445

Met Ser Phe Thr Glu Phe Pro Lys Asp Leu Pro Ser Ala Val Val Asn
    450                 455                 460

Arg Glu Arg Leu Leu Gln Leu Trp Thr Asn Phe Ala Lys Thr Gly Asn
465                 470                 475                 480

Pro Thr Pro Glu Ile Asn Asp Val Ile Thr Thr Lys Trp Asp Lys Ala
                485                 490                 495
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Thr Glu Glu Lys Ser Asp His Met Asp Ile Asp Asn Thr Leu Arg Met
500 505 510

Ile Pro Asp Pro Asp Ala Lys Arg Leu Arg Phe Trp Asn Lys Phe Leu
515 520 525

<210> 38
<211> 2007
<212> DNA
<213> Ctenocephalides felis

<400> 38
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aaaaaaaaat gaaaaaataa aagcaaatat gatacaaaga tggtaataat atcaaatata 120

aataatgtgg cgtccattaa tcacattttt agttcagttc ttcaagaaga gcgacaaatt 180

taggcacagt acaccatctg ttgaatgcgc aaatcactaa aacagaattt gttctaaatt 240

taccacctac ttcttgatta ttacaactgt aaaagctttt tttccaataa tcagagtaaa 300

tttgaaatcg aaatatactt caattagagc caattgaatc tcgtacatct aaacgtgata 360

attatactaa tacagaaact ctataataaa atcgataatt ggtatattta tcataaaaat 420

ttattccaaa atctaagtcg ttttgcatca ggatctggaa tcattctcaa agtattatcg 480

atatccatat gatctgattt ttcctcagta gctttatccc attttgttgt tataacatca 540

ttgatttcag gagtgggatt tcctgttttt gcaaaatttg tccaaagttg caacaatcgt 600

tccctattca ccactgcact tggtaaatct tttggaaatt ctgtaaaact catcttgaaa 660

agatatccca gctcatctcc atgagctgct ccttcaatat taggatctaa tacaagtttc 720

ttcaaaaaac caaaatcatc aaaactataa acatataaat ataacggttc tgaggaatgt 780

tcaattatat atcttgcagt atttttaatc cctctcaaaa accaagtatc actaataaca 840

ctgacaaatt tttctttgtt gtctgaagaa acaggttcgt cttggtaata aaactttctc 900

atttcttcag ccaatttttt agattcctta gaccttaaag ttagattcaa atctactggt 960

acaaatcttt caaaatcagc ttcaaacttc tcaaatatat ttgggtcatc cttgaagtcc 1020

attaaaccta aaattccttc agcactgttg tatccacata taaatgggac ttttgtgaaa 1080

ttgcctgatt gcatttttga taatggagac tggtccaaga atggttcaaa attttgataa 1140

cgtttttcta ttgttggtag aaaaggatag tctataataa gttggccttt gtcttttggt 1200

tttattctgt tgtctataag atcatctatg ggggcttgac gaaggatttt tagagcttct 1260

gtctcgttat cgacaggatg acccagaagt ttgcagaggc ggaatgcatt ttctttatta 1320

ttatcatgtt gaagtgccca aggattaaaa gcacttccac tttgtgagat cgctttatga 1380

aaaagtcctt tggaaagatc tgataacatc aaataatgaa cacttgcacc acctgctgat 1440

tctccaaaaa tagtcacatt gttggggtca ccaccaaagg atgcaatatt gtttttttacc 1500

cattttagag cttcaacctg gtccatcaaa ccaacattgc caggcgcttc ttctattccc 1560

aggttcaaaa atcccaaaac acctaatcga taattgaaag taaccagaac aattccataa 1620

tccatcaaat attcaggacc atacatatca ctatttccag atcccatgaa gaagcctcct 1680

ccatgtatcc ataccattac tggaagaagt gatttctctg atgtttttgg tacatagaca 1740

ttgaggtata aacaatcttc agcccctact ttaatttttt taataaaatg tactgatcta 1800

caactattcc cttctttact agcatcaaga acacctgacc aaggttctgc aggttgaggt 1860

ggcttaaatc ttagatcacc tacaggaggt ttggcatatg gaattccaga ataactatgg 1920

aacacatttc ctttttcact aatttgctct tttcctttta aagtaccttg aagcaaagtc 1980

acttgtagat cagccatcgt tggaact 2007

<210> 39
<211> 12
<212> PRT
<213> Peptide

<400> 39

Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu
1 5 10

<210> 40
<211> 22
<212> PRT
<213> Peptide

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> Xaa = unknown

<400> 40

Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu Val Gly Lys Ala
1 5 10 15

Thr Asn Glu Asn Xaa Lys
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<210> 41
<211> 12
<212> PRT
<213> Peptide

<400> 41

Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu
1 5 10

<210> 42
<211> 21

<212> PRT
<213> Peptide

<400> 42

Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu Val Gly Lys Ala
1 5 10 15

Leu Ser Asn Glu Asn
20

<210> 43
<211> 8
<212> PRT
<213> Peptide

<400> 43

Asp Pro Pro Thr Val Thr Leu Pro
1 5

<210> 44
<211> 23
<212> PRT
<213> Peptide

<400> 44

Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu Val Gly Lys Ala
1 5 10 15

Leu Thr Asn Glu Asn Gly Lys
20

<210> 45
<211> 20
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<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 45
aattaaccct cactaaaggg 20

<210> 46
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 46
ardccdccdc crtrdat 17

<210> 47

<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 47
tgtgctcgag atgggataac ctagatcagc atttgtgc 38

<210> 48
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 48
ttaaggtacc tcatctaata cttccttcat tacag 35

<210> 49
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 49
aaaactgcag tataaatatg ttacctcaca gtagtg 36

<210> 50
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 50
tgctctagat tatctaatac ttccttcatt acag 34

<210> 51
<211> 1584
<212> DNA
<213> Ctenocephalides felis

<220>
<221> exon
<222> (1)..(1584)
<223>

<400> 51
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Met Ala Asp Leu Gln Val Thr Leu Leu Gln Gly Thr Leu Lys Gly Lys
1 5 10 15

gag caa att agt gaa aaa gga aat gtg ttc cat agt tat tct gga att 96

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Glu Gln Ile Ser Glu Lys Gly Asn Val Phe His Ser Tyr Ser Gly Ile
            20                  25                  30

cca tat gcc aaa cct cct gta ggt gat cta aga ttt aag cca cct caa      144
Pro Tyr Ala Lys Pro Pro Val Gly Asp Leu Arg Phe Lys Pro Pro Gln
        35                  40                  45

cct gca gaa cct tgg tca ggt gtt ctt gat gct agt aaa gaa ggg aat      192
Pro Ala Glu Pro Trp Ser Gly Val Leu Asp Ala Ser Lys Glu Gly Asn
    50                  55                  60

agt tgt aga tca gta cat ttt att aaa aaa att aaa gta ggg gct gaa      240
Ser Cys Arg Ser Val His Phe Ile Lys Lys Ile Lys Val Gly Ala Glu
65                  70                  75                  80

gat tgt tta tac ctc aat gtc tat gta cca aaa aca tca gag aaa tca      288
Asp Cys Leu Tyr Leu Asn Val Tyr Val Pro Lys Thr Ser Glu Lys Ser
                85                  90                  95

ctt ctt cca gta atg gta tgg ata cat gga gga ggc ttc ttc atg gga      336
Leu Leu Pro Val Met Val Trp Ile His Gly Gly Gly Phe Phe Met Gly
            100                 105                 110

tct gga aat agt gat atg tat ggt cct gaa tat ttg atg gat tat gga      384
Ser Gly Asn Ser Asp Met Tyr Gly Pro Glu Tyr Leu Met Asp Tyr Gly
        115                 120                 125

att gtt ctg gtt act ttc aat tat cga tta ggt gtt ttg gga ttt ttg      432
Ile Val Leu Val Thr Phe Asn Tyr Arg Leu Gly Val Leu Gly Phe Leu
    130                 135                 140

aac ctg gga ata gaa gaa gcg cct ggc aat gtt ggt ttg atg gac cag      480
Asn Leu Gly Ile Glu Glu Ala Pro Gly Asn Val Gly Leu Met Asp Gln
145                 150                 155                 160

gtt gaa gct cta aaa tgg gta aaa aac aat att gca tcc ttt ggt ggt      528
Val Glu Ala Leu Lys Trp Val Lys Asn Asn Ile Ala Ser Phe Gly Gly
                165                 170                 175

gac ccc aac aat gtg act att ttt gga gaa tca gca ggt ggt gca agt      576
Asp Pro Asn Asn Val Thr Ile Phe Gly Glu Ser Ala Gly Gly Ala Ser
            180                 185                 190

gtt cat tat ttg atg tta tca gat ctt tcc aaa gga ctt ttt cat aaa      624
Val His Tyr Leu Met Leu Ser Asp Leu Ser Lys Gly Leu Phe His Lys
        195                 200                 205

gcg atc tca caa agt gga agt gct ttt aat cct tgg gca ctt caa cat      672
Ala Ile Ser Gln Ser Gly Ser Ala Phe Asn Pro Trp Ala Leu Gln His
    210                 215                 220

gat aat aat aaa gaa aat gca ttc cgc ctc tgc aaa ctt ctg ggt cat      720
Asp Asn Asn Lys Glu Asn Ala Phe Arg Leu Cys Lys Leu Leu Gly His
225                 230                 235                 240

cct gtc gat aac gag aca gaa gct cta aaa atc ctt cgt caa gcc ccc      768
Pro Val Asp Asn Glu Thr Glu Ala Leu Lys Ile Leu Arg Gln Ala Pro
                245                 250                 255

ata gat gat ctt ata gac aac aga ata aaa cca aaa gac aaa ggc caa      816
Ile Asp Asp Leu Ile Asp Asn Arg Ile Lys Pro Lys Asp Lys Gly Gln
            260                 265                 270

ctt att ata gac tat cct ttt cta cca aca ata gaa aaa cgt tat caa      864
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Leu Ile Ile Asp Tyr Pro Phe Leu Pro Thr Ile Glu Lys Arg Tyr Gln
        275                 280                 285

aat ttt gaa cca ttc ttg gac cag tct cca tta tca aaa atg caa tca      912
Asn Phe Glu Pro Phe Leu Asp Gln Ser Pro Leu Ser Lys Met Gln Ser
    290                 295                 300

ggc aat ttc aca aaa gtc cca ttt ata tgt gga tac aac agt gct gaa      960
Gly Asn Phe Thr Lys Val Pro Phe Ile Cys Gly Tyr Asn Ser Ala Glu
305                 310                 315                 320

gga att tta ggt tta atg gac ttc aag gat gac cca aat ata ttt gag     1008
Gly Ile Leu Gly Leu Met Asp Phe Lys Asp Asp Pro Asn Ile Phe Glu
                325                 330                 335

aag ttt gaa gct gat ttt gaa aga ttt gta cca gta gat ttg aat cta     1056
Lys Phe Glu Ala Asp Phe Glu Arg Phe Val Pro Val Asp Leu Asn Leu
            340                 345                 350

act tta agg tct aag gaa tct aaa aaa ttg gct gaa gaa atg aga aag     1104
Thr Leu Arg Ser Lys Glu Ser Lys Lys Leu Ala Glu Glu Met Arg Lys
        355                 360                 365

ttt tat tac caa gac gaa cct gtt tct tca gac aac aaa gaa aaa ttt     1152
Phe Tyr Tyr Gln Asp Glu Pro Val Ser Ser Asp Asn Lys Glu Lys Phe
    370                 375                 380

gtc agt gtt att agt gat act tgg ttt ttg aga ggg att aaa aat act     1200
Val Ser Val Ile Ser Asp Thr Trp Phe Leu Arg Gly Ile Lys Asn Thr
385                 390                 395                 400

gca aga tat ata att gaa cat tcc tca gaa ccg tta tat tta tat gtt     1248
Ala Arg Tyr Ile Ile Glu His Ser Ser Glu Pro Leu Tyr Leu Tyr Val
                405                 410                 415

tat agt ttt gat gat ttt ggt ttt ttg aag aaa ctt gta tta gat cct     1296
Tyr Ser Phe Asp Asp Phe Gly Phe Leu Lys Lys Leu Val Leu Asp Pro
            420                 425                 430

aat att gaa gga gca gct cat gga gat gag ctg gga tat ctt ttc aag     1344
Asn Ile Glu Gly Ala Ala His Gly Asp Glu Leu Gly Tyr Leu Phe Lys
        435                 440                 445

atg agt ttt aca gaa ttt cca aaa gat tta cca agt gca gtg gtg aat     1392
Met Ser Phe Thr Glu Phe Pro Lys Asp Leu Pro Ser Ala Val Val Asn
    450                 455                 460

agg gaa cga ttg ttg caa ctt tgg aca aat ttt gca aaa aca gga aat     1440
Arg Glu Arg Leu Leu Gln Leu Trp Thr Asn Phe Ala Lys Thr Gly Asn
465                 470                 475                 480

ccc act cct gaa atc aat gat gtt ata aca aca aaa tgg gat aaa gct     1488
Pro Thr Pro Glu Ile Asn Asp Val Ile Thr Thr Lys Trp Asp Lys Ala
                485                 490                 495

act gag gaa aaa tca gat cat atg gat atc gat aat act ttg aga atg     1536
Thr Glu Glu Lys Ser Asp His Met Asp Ile Asp Asn Thr Leu Arg Met
            500                 505                 510

att cca gat cct gat gca aaa cga ctt aga ttt tgg aat aaa ttt tta     1584
Ile Pro Asp Pro Asp Ala Lys Arg Leu Arg Phe Trp Asn Lys Phe Leu
        515                 520                 525
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<210> 52
<211> 1584
<212> DNA
<213> Ctenocephalides felis

<400> 52
taaaaattta ttccaaaatc taagtcgttt tgcatcagga tctggaatca ttctcaaagt 60

attatcgata tccatatgat ctgatttttc ctcagtagct ttatcccatt ttgttgttat 120

aacatcattg atttcaggag tgggatttcc tgtttttgca aaatttgtcc aaagttgcaa 180

caatcgttcc ctattcacca ctgcacttgg taaatctttt ggaaattctg taaaactcat 240

cttgaaaaga tatcccagct catctccatg agctgctcct tcaatattag gatctaatac 300

aagtttcttc aaaaaaccaa aatcatcaaa actataaaca tataaatata acggttctga 360

ggaatgttca attatatatc ttgcagtatt tttaatccct ctcaaaaacc aagtatcact 420

aataacactg acaaattttt ctttgttgtc tgaagaaaca ggttcgtctt ggtaataaaa 480

ctttctcatt tcttcagcca atttttttaga ttccttagac cttaaagtta gattcaaatc 540

tactggtaca aatctttcaa aatcagcttc aaacttctca aatatatttg ggtcatcctt 600

gaagtccatt aaacctaaaa ttccttcagc actgttgtat ccacatataa atgggacttt 660

tgtgaaattg cctgattgca tttttgataa tggagactgg tccaagaatg gttcaaaatt 720

ttgataacgt ttttctattg ttggtagaaa aggatagtct ataataagtt ggcctttgtc 780

ttttggtttt attctgttgt ctataagatc atctatgggg gcttgacgaa ggatttttag 840

agcttctgtc tcgttatcga caggatgacc cagaagtttg cagaggcgga atgcattttc 900

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tttatgaaaa agtcctttgg aaagatctga taacatcaaa taatgaacac ttgcaccacc 1020

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ttttacccat tttagagctt caacctggtc catcaaacca acattgccag gcgcttcttc 1140

tattcccagg ttcaaaaatc ccaaaacacc taatcgataa ttgaaagtaa ccagaacaat 1200

tccataatcc atcaaatatt caggaccata catatcacta tttccagatc ccatgaagaa 1260

gcctcctcca tgtatccata ccattactgg aagaagtgat ttctctgatg tttttggtac 1320

atagacattg aggtataaac aatcttcagc ccctacttta attttttttaa taaaatgtac 1380

tgatctacaa ctattccctt ctttactagc atcaagaaca cctgaccaag gttctgcagg 1440

ttgaggtggc ttaaatctta gatcacctac aggaggtttg gcatatggaa ttccagaata 1500

actatggaac acatttcctt tttcactaat ttgctctttt ccttttaaag taccttgaag 1560

caaagtcact tgtagatcag ccat 1584

<210> 53
<211> 530
<212> PRT

<213> Ctenocephalides felis

<400> 53

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Asp Pro Pro Thr Val Thr Leu Pro Gln Gly Glu Leu Val Gly Lys Ala
1               5                  10                  15

Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr Thr Gly Val Pro
            20                  25                  30

Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys Pro Pro Gln Lys
        35                  40                  45

Ala Glu Pro Trp Asn Gly Val Phe Asn Ala Thr Ser His Gly Asn Val
    50                  55                  60

Cys Lys Ala Leu Asn Phe Phe Leu Lys Lys Ile Glu Gly Asp Glu Asp
65                  70                  75                  80

Cys Leu Leu Val Asn Val Tyr Ala Pro Lys Thr Thr Ser Asp Lys Lys
                85                  90                  95

Leu Pro Val Phe Phe Trp Val His Gly Gly Gly Phe Val Thr Gly Ser
            100                 105                 110

Gly Asn Leu Glu Phe Gln Ser Pro Asp Tyr Leu Val Asn Tyr Asp Val
        115                 120                 125

Ile Phe Val Thr Phe Asn Tyr Arg Leu Gly Pro Leu Gly Phe Leu Asn
    130                 135                 140

Leu Glu Leu Glu Gly Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Val
145                 150                 155                 160

Ala Ala Leu Lys Trp Thr Lys Glu Asn Ile Glu Lys Phe Gly Gly Asp
                165                 170                 175

Pro Glu Asn Ile Thr Ile Gly Gly Val Ser Ala Gly Gly Ala Ser Val
            180                 185                 190

His Tyr Leu Leu Leu Ser His Thr Thr Thr Gly Leu Tyr Lys Arg Ala
        195                 200                 205

Ile Ala Gln Ser Gly Ser Ala Leu Asn Pro Trp Ala Phe Gln Arg His
    210                 215                 220

Pro Val Lys Arg Ser Leu Gln Leu Ala Glu Ile Leu Gly His Pro Thr
225                 230                 235                 240
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Asn Asn Thr Gln Asp Ala Leu Glu Phe Leu Gln Lys Ala Pro Val Asp
                245                 250                 255

Ser Leu Leu Lys Lys Met Pro Ala Glu Thr Glu Gly Glu Ile Ile Glu
            260                 265                 270

Glu Phe Val Phe Val Pro Ser Ile Glu Lys Val Phe Pro Ser His Gln
        275                 280                 285

Pro Phe Leu Glu Glu Ser Pro Leu Ala Arg Met Lys Ser Gly Ser Phe
    290                 295                 300

Asn Lys Val Pro Leu Leu Val Gly Phe Asn Ser Ala Glu Gly Leu Leu
305                 310                 315                 320

Tyr Lys Phe Phe Met Lys Glu Lys Pro Glu Met Leu Asn Gln Ala Glu
                325                 330                 335

Ala Asp Phe Glu Arg Leu Val Pro Ala Glu Phe Glu Leu Ala His Gly
            340                 345                 350

Ser Glu Glu Ser Lys Lys Leu Ala Glu Lys Ile Arg Lys Phe Tyr Phe
        355                 360                 365

Asp Asp Lys Pro Val Pro Glu Asn Glu Gln Lys Phe Ile Asp Leu Ile
    370                 375                 380

Gly Asp Ile Trp Phe Thr Arg Gly Ile Asp Lys His Val Lys Leu Ser
385                 390                 395                 400

Val Glu Lys Gln Asp Glu Pro Val Tyr Tyr Tyr Glu Tyr Ser Phe Ser
                405                 410                 415

Glu Ser His Pro Ala Lys Gly Thr Phe Gly Asp His Asn Leu Thr Gly
            420                 425                 430

Ala Cys His Gly Glu Glu Leu Val Asn Leu Phe Lys Val Glu Met Met
        435                 440                 445

Lys Leu Glu Lys Asp Lys Pro Asn Val Leu Leu Thr Lys Asp Arg Val
    450                 455                 460

Leu Ala Met Trp Thr Asn Phe Ile Lys Asn Gly Asn Pro Thr Pro Glu
465                 470                 475                 480

Val Thr Glu Leu Leu Pro Val Lys Trp Glu Pro Ala Thr Lys Asp Lys
                485                 490                 495
```

Leu Asn Tyr Leu Asn Ile Asp Ala Thr Leu Thr Leu Gly Thr Asn Pro
500 505 510

Glu Glu Thr Arg Val Lys Phe Trp Glu Asp Ala Thr Lys Thr Leu His
515 520 525

Ser Gln
530

<210> 54
<211> 570
<212> PRT
<213> Ctenocephalides felis

<400> 54

Trp Asp Asn Leu Asp Gln His Leu Cys Arg Val Gln Phe Asn Gly Ile
1 5 10 15

Thr Glu Gly Lys Pro Phe Arg Tyr Lys Asp His Arg Asn Asp Val Tyr
20 25 30

Cys Ser Tyr Leu Gly Ile Pro Tyr Ala Glu Pro Pro Phe Gly Pro Leu
35 40 45

Arg Phe Gln Ser Pro Lys Pro Ile Ser Asn Pro Lys Thr Gly Phe Val
50 55 60

Gln Ala Arg Thr Leu Gly Asp Lys Cys Phe Gln Glu Ser Leu Ile Tyr
65 70 75 80

Ser Tyr Ala Gly Ser Glu Asp Cys Leu Tyr Leu Asn Ile Phe Thr Pro
85 90 95

Glu Thr Val Asn Ser Ala Asn Asn Thr Lys Tyr Pro Val Met Phe Trp
100 105 110

Ile His Gly Gly Ala Phe Asn Gln Gly Ser Gly Ser Tyr Asn Phe Phe
115 120 125

Gly Pro Asp Tyr Leu Ile Arg Glu Gly Ile Ile Leu Val Thr Ile Asn
130 135 140

Tyr Arg Leu Gly Val Phe Gly Phe Leu Ser Ala Pro Glu Trp Asp Ile
145 150 155 160

His Gly Asn Met Gly Leu Lys Asp Gln Arg Leu Ala Leu Lys Trp Val
165 170 175

Tyr Asp Asn Ile Glu Lys Phe Gly Gly Asp Arg Glu Lys Ile Thr Ile

180 185 190

Ala Gly Glu Ser Ala Gly Ala Ala Ser Val His Phe Leu Met Met Asp
195 200 205

Asn Ser Thr Arg Lys Tyr Tyr Gln Arg Ala Ile Leu Gln Ser Gly Thr
210 215 220

Leu Leu Asn Pro Thr Ala Asn Gln Ile Gln Leu Leu His Arg Phe Glu
225 230 235 240

Lys Leu Lys Gln Val Leu Asn Ile Thr Gln Lys Gln Glu Leu Leu Asn
245 250 255

Leu Asp Lys Asn Leu Ile Leu Arg Ala Ala Leu Asn Arg Val Pro Asp
260 265 270

Ser Asn Asp His Asp Arg Asp Thr Val Pro Val Phe Asn Pro Val Leu
275 280 285

Glu Ser Pro Glu Ser Pro Asp Pro Ile Thr Phe Pro Ser Ala Leu Glu
290 295 300

Arg Met Arg Asn Gly Glu Phe Pro Asp Val Asp Val Ile Ile Gly Phe
305 310 315 320

Asn Ser Ala Glu Gly Leu Arg Ser Met Ala Arg Val Thr Arg Gly Asn
325 330 335

Met Glu Val His Lys Thr Leu Thr Asn Ile Glu Arg Ala Ile Pro Arg
340 345 350

Asp Ala Asn Ile Trp Lys Asn Pro Asn Gly Ile Glu Glu Lys Lys Leu
355 360 365

Ile Lys Met Leu Thr Glu Phe Tyr Asp Gln Val Lys Glu Gln Asn Asp
370 375 380

Asp Ile Glu Ala Tyr Val Gln Leu Lys Gly Asp Ala Gly Tyr Leu Gln
385 390 395 400

Gly Ile Tyr Arg Thr Leu Lys Ala Ile Phe Phe Asn Glu Phe Arg Arg
405 410 415

Asn Ser Asn Leu Tyr Leu Tyr Arg Leu Ser Asp Asp Thr Tyr Ser Val
420 425 430

Tyr Lys Ser Tyr Ile Leu Pro Tyr Arg Trp Gly Ser Leu Pro Gly Val

435 440 445

Ser His Gly Asp Asp Leu Gly Tyr Leu Phe Ala Asn Ser Leu Asp Val
450 455 460

Pro Ile Leu Gly Thr Thr His Ile Ser Ile Pro Gln Asp Ala Met Gln
465 470 475 480

Thr Leu Glu Arg Met Val Arg Ile Trp Thr Asn Phe Val Lys Asn Gly
485 490 495

Lys Pro Thr Ser Asn Thr Glu Asp Ala Ser Cys Asp Thr Lys Arg His
500 505 510

Leu Asn Asp Ile Phe Trp Glu Pro Tyr Asn Asp Glu Glu Pro Lys Tyr
515 520 525

Leu Asp Met Gly Lys Glu Asn Phe Glu Met Lys Asn Ile Leu Glu Leu
530 535 540

Lys Arg Met Met Leu Trp Asp Glu Val Tyr Arg Asn Ala Asn Leu Arg
545 550 555 560

Phe Arg Val Cys Asn Glu Gly Ser Ile Arg
565 570

<210> 55
<211> 570
<212> PRT
<213> Ctenocephalides felis

<400> 55

Trp Asp Asn Leu Asp Gln His Leu Cys Arg Val Gln Phe Asn Gly Ile
1 5 10 15

Thr Glu Gly Lys Pro Phe Arg Tyr Lys Asp His Lys Asn Asp Val Tyr
20 25 30

Cys Ser Tyr Leu Gly Ile Pro Tyr Ala Glu Pro Pro Ile Gly Pro Leu
35 40 45

Arg Phe Gln Ser Pro Lys Pro Ile Ser Asn Pro Lys Thr Gly Phe Val
50 55 60

Gln Ala Arg Ser Leu Gly Asp Lys Cys Phe Gln Glu Ser Leu Ile Tyr
65 70 75 80

Ser Tyr Ala Gly Ser Glu Asp Cys Leu Tyr Leu Asn Ile Phe Thr Pro
85 90 95

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Glu Thr Val Asn Ser Ala Asn Asn Thr Lys Tyr Pro Val Met Phe Trp
            100                 105                 110

Ile His Gly Gly Ala Phe Asn Gln Gly Ser Gly Ser Tyr Asn Phe Phe
        115                 120                 125

Gly Pro Asp Tyr Leu Ile Arg Glu Gly Ile Ile Leu Val Thr Ile Asn
    130                 135                 140

Tyr Arg Leu Gly Val Phe Gly Phe Leu Ser Ala Pro Glu Trp Asp Ile
145                 150                 155                 160

His Gly Asn Met Gly Leu Lys Asp Gln Arg Leu Ala Leu Lys Trp Val
                165                 170                 175

Tyr Asp Asn Ile Glu Lys Phe Gly Gly Asp Arg Asp Lys Ile Thr Ile
            180                 185                 190

Ala Gly Glu Ser Ala Gly Ala Ala Ser Val His Phe Leu Met Met Asp
        195                 200                 205

Asn Ser Thr Arg Lys Tyr Tyr Gln Arg Ala Ile Leu Gln Ser Gly Thr
    210                 215                 220

Leu Leu Asn Pro Thr Ala Asn Gln Ile Gln Pro Leu His Arg Phe Glu
225                 230                 235                 240

Lys Leu Lys Gln Val Leu Asn Ile Thr Gln Lys Gln Glu Leu Leu Asn
                245                 250                 255

Leu Asp Lys Asn Gln Ile Leu Arg Ala Ala Leu Asn Arg Val Pro Asp
            260                 265                 270

Asn Asn Asp His Glu Arg Asp Thr Val Pro Val Phe Asn Pro Val Leu
        275                 280                 285

Glu Ser Pro Glu Ser Pro Asp Pro Ile Thr Phe Pro Ser Ala Leu Glu
    290                 295                 300

Arg Met Arg Asn Gly Glu Phe Pro Asp Val Asp Val Ile Ile Gly Phe
305                 310                 315                 320

Asn Ser Ala Glu Gly Leu Arg Ser Met Pro Arg Val Thr Arg Gly Asn
                325                 330                 335

Met Glu Val Tyr Lys Thr Leu Thr Asn Ile Glu Arg Ala Ile Pro Arg
            340                 345                 350
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Asp Ala Asn Ile Trp Lys Asn Pro Asn Gly Ile Glu Glu Lys Lys Leu
        355                 360                 365

Ile Lys Met Leu Thr Glu Phe Tyr Asp Gln Val Lys Glu Gln Asn Asp
    370                 375                 380

Asp Ile Glu Ala Tyr Val Gln Leu Lys Gly Asp Ala Gly Tyr Leu Gln
385                 390                 395                 400

Gly Ile Tyr Arg Thr Leu Lys Ala Ile Phe Phe Asn Glu Ile Lys Arg
                405                 410                 415

Asn Ser Asn Leu Tyr Leu Tyr Arg Leu Ser Asp Asp Thr Tyr Ser Val
            420                 425                 430

Tyr Lys Ser Tyr Ile Leu Pro Tyr Arg Trp Gly Ser Leu Pro Gly Val
        435                 440                 445

Ser His Gly Asp Asp Leu Gly Tyr Leu Phe Ala Asn Ser Leu Asp Val
    450                 455                 460

Pro Ile Leu Gly Thr Thr His Ile Ser Ile Pro Gln Asp Ala Met Gln
465                 470                 475                 480

Thr Leu Glu Arg Met Val Arg Ile Trp Thr Asn Phe Val Lys Asn Gly
                485                 490                 495

Lys Pro Thr Ser Asn Thr Glu Asp Ala Ser Cys Asp Thr Lys Arg His
            500                 505                 510

Leu Asn Asp Ile Phe Trp Glu Pro Tyr Asn Asp Glu Glu Pro Lys Tyr
        515                 520                 525

Leu Asp Met Gly Lys Glu His Phe Glu Met Lys Asn Ile Leu Glu Leu
    530                 535                 540

Lys Arg Met Met Leu Trp Asp Glu Val Tyr Arg Asn Ala Asn Leu Arg
545                 550                 555                 560

Phe Arg Val Cys Asn Glu Gly Ser Ile Arg
                565                 570
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<210> 56
<211> 20
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic Primer

<400> 56
gtgcgtacac gtttactacc 20

<210> 57
<211> 2144
<212> DNA
<213> Ctenocephalides felis

<220>
<221> CDS
<222> (30)..(1682)
<223>

<220>
<221> misc_feature
<222> (462)..(462)
<223> At nucleotide 462, r = a or g
At amino acid residue 145, Xaa = Asn or Asp

<400> 57
gtacacatag tcaatagtct agatccaag atg tct cgt gtt att ttt tta agt 53
Met Ser Arg Val Ile Phe Leu Ser
1 5

tgt att ttt ttg ttt agt ttt aat ttt ata aaa tgt gat tcc ccg act 101
Cys Ile Phe Leu Phe Ser Phe Asn Phe Ile Lys Cys Asp Ser Pro Thr
10 15 20

gta act ttg ccc caa ggc gaa ttg gtt gga aaa gct ttg acg aac gaa 149
Val Thr Leu Pro Gln Gly Glu Leu Val Gly Lys Ala Leu Thr Asn Glu
25 30 35 40

aat gga aaa gag tat ttt agc tac aca ggt gta cct tat gct aaa cct 197
Asn Gly Lys Glu Tyr Phe Ser Tyr Thr Gly Val Pro Tyr Ala Lys Pro
45 50 55

cct gtt gga gaa ctt aga ttt aag cct cca cag aaa gct gag cca tgg 245
Pro Val Gly Glu Leu Arg Phe Lys Pro Pro Gln Lys Ala Glu Pro Trp
60 65 70

caa ggt gtt ttc aac gcc aca tta tac gga aat gtg tgt aaa tct tta 293
Gln Gly Val Phe Asn Ala Thr Leu Tyr Gly Asn Val Cys Lys Ser Leu
75 80 85

aat ttc ttc ttg aag aaa att gaa gga gac gaa gac tgc ttg gta gta 341
Asn Phe Phe Leu Lys Lys Ile Glu Gly Asp Glu Asp Cys Leu Val Val
90 95 100

aac gtg tac gca cca aaa aca act tct gat aaa aaa ctt cca gta ttt 389
Asn Val Tyr Ala Pro Lys Thr Thr Ser Asp Lys Lys Leu Pro Val Phe
105 110 115 120

ttc tgg gtt cat ggt ggt ggt ttt gtg act gga tcc gga aat tta gaa 437
Phe Trp Val His Gly Gly Gly Phe Val Thr Gly Ser Gly Asn Leu Glu
125 130 135

ttc caa agc cca gat tat tta gta rat ttt gat gtt att ttc gta act 485
Phe Gln Ser Pro Asp Tyr Leu Val Xaa Phe Asp Val Ile Phe Val Thr
140 145 150

```
ttc aat tac cga ttg gga cct ctc gga ttt ctg aat ttg gag ttg gag      533
Phe Asn Tyr Arg Leu Gly Pro Leu Gly Phe Leu Asn Leu Glu Leu Glu
        155                 160                 165

ggt gct cca gga aat gta gga tta ttg gat cag gtg gca gct ctg aaa      581
Gly Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Val Ala Ala Leu Lys
    170                 175                 180

tgg acc aaa gaa aac att gag aaa ttt ggt gga gat cca gaa aat att      629
Trp Thr Lys Glu Asn Ile Glu Lys Phe Gly Gly Asp Pro Glu Asn Ile
185                 190                 195                 200

aca att ggt ggt gtt tct gct ggt gga gca agt gtt cat tat ctt ttg      677
Thr Ile Gly Gly Val Ser Ala Gly Gly Ala Ser Val His Tyr Leu Leu
                205                 210                 215

tta tct cat aca acc act gga ctt tac aaa agg gca att gct caa agt      725
Leu Ser His Thr Thr Thr Gly Leu Tyr Lys Arg Ala Ile Ala Gln Ser
            220                 225                 230

gga agt gct ttt aat cca tgg gcc ttc caa aga cat cca gta aag cgt      773
Gly Ser Ala Phe Asn Pro Trp Ala Phe Gln Arg His Pro Val Lys Arg
        235                 240                 245

agt ctt caa ctt gct gag ata ttg ggt cat ccc aca aac aat act caa      821
Ser Leu Gln Leu Ala Glu Ile Leu Gly His Pro Thr Asn Asn Thr Gln
    250                 255                 260

gat gct tta gaa ttc tta caa aaa gcc ccc gta gac agt ctc ctg aag      869
Asp Ala Leu Glu Phe Leu Gln Lys Ala Pro Val Asp Ser Leu Leu Lys
265                 270                 275                 280

aaa atg cca gct gaa aca gaa ggt gaa ata ata gaa gag ttt gtc ttc      917
Lys Met Pro Ala Glu Thr Glu Gly Glu Ile Ile Glu Glu Phe Val Phe
                285                 290                 295

gta cca tca att gaa aaa gtt ttc cca tcc cac caa cct ttc ttg gaa      965
Val Pro Ser Ile Glu Lys Val Phe Pro Ser His Gln Pro Phe Leu Glu
            300                 305                 310

gaa tca cca ttg gcc aga atg aaa tcc gga tcc ttt aac aaa gta cct     1013
Glu Ser Pro Leu Ala Arg Met Lys Ser Gly Ser Phe Asn Lys Val Pro
        315                 320                 325

tta tta gtt gga ttt aac agt gca gaa gga ctt ttg ttc aaa ttc ttc     1061
Leu Leu Val Gly Phe Asn Ser Ala Glu Gly Leu Leu Phe Lys Phe Phe
    330                 335                 340

atg aaa gaa aaa cca gag atg ctg aac caa gct gaa gca gat ttt gaa     1109
Met Lys Glu Lys Pro Glu Met Leu Asn Gln Ala Glu Ala Asp Phe Glu
345                 350                 355                 360

aga ctc gta cca gcc gaa ttt gaa tta gtc cat gga tca gag gaa tcg     1157
Arg Leu Val Pro Ala Glu Phe Glu Leu Val His Gly Ser Glu Glu Ser
                365                 370                 375

aaa aaa ctt gca gaa aaa atc agg aag ttt tac ttt gac gat aaa ccc     1205
Lys Lys Leu Ala Glu Lys Ile Arg Lys Phe Tyr Phe Asp Asp Lys Pro
            380                 385                 390

gtt cca gaa aat gaa cag aaa ttt att gac ttg ata gga gat att tgg     1253
Val Pro Glu Asn Glu Gln Lys Phe Ile Asp Leu Ile Gly Asp Ile Trp
        395                 400                 405
```

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ttt act aga ggt gtt gac aag cat gtc aag ttg tct gtg gag aaa caa     1301
Phe Thr Arg Gly Val Asp Lys His Val Lys Leu Ser Val Glu Lys Gln
    410                 415                 420

gac gaa cca gtt tat tat tat gaa tat tcc ttc tcg gaa agt cat cct     1349
Asp Glu Pro Val Tyr Tyr Tyr Glu Tyr Ser Phe Ser Glu Ser His Pro
425                 430                 435                 440

gca aaa gga aca ttt ggt gat cat aat ctg act ggt gca tgc cat gga     1397
Ala Lys Gly Thr Phe Gly Asp His Asn Leu Thr Gly Ala Cys His Gly
                445                 450                 455

gaa gaa ctt gtg aat tta ttc aaa gtc gag atg atg aag ctg gaa aaa     1445
Glu Glu Leu Val Asn Leu Phe Lys Val Glu Met Met Lys Leu Glu Lys
            460                 465                 470

gat aaa cct aat gtt cta tta aca aaa gat aga gta ctt gcc atg tgg     1493
Asp Lys Pro Asn Val Leu Leu Thr Lys Asp Arg Val Leu Ala Met Trp
        475                 480                 485

act aac ttc atc aaa aat gga aat cct act cct gaa gta aca gaa tta     1541
Thr Asn Phe Ile Lys Asn Gly Asn Pro Thr Pro Glu Val Thr Glu Leu
    490                 495                 500

ttg cca gtt aaa tgg gaa cct gcc aca aaa gac aag ttg aat tat ttg     1589
Leu Pro Val Lys Trp Glu Pro Ala Thr Lys Asp Lys Leu Asn Tyr Leu
505                 510                 515                 520

aac att gat gcc acc tta act ttg gga aca aat cct gag gca aac cga     1637
Asn Ile Asp Ala Thr Leu Thr Leu Gly Thr Asn Pro Glu Ala Asn Arg
                525                 530                 535

gtc aaa ttt tgg gaa gac gcc aca aaa tct ttg cac ggt caa taa         1682
Val Lys Phe Trp Glu Asp Ala Thr Lys Ser Leu His Gly Gln
            540                 545                 550

taatttatga aaattgtttt aaatacttta ggtaatatat taggtaaata aaaattaaaa   1742

ataacaattt tttatgtttt atgtattggc ttatgtgtat cagttctaat tttatttatt   1802

tattcttgtt ttgcttgttt tgaaatatca tggttttaat tttcaaaaca caacgtcgtt   1862

tgtttttagc aaaatttcca atagatatgt tatattaagt actctgaagt atttttatat   1922

atacactaaa atcagtaaaa atacattaac taaaaatata agatattttc aataatttttt  1982

tttaaagaaa ataccaaaaa taaagtaaaa ttccaaacgg aatttttgtt taacttaaaa   2042

ataaaattaa ctcttcaata attttgataa ttagtatttc tgatatcatt agtgaaaatt   2102

atattttgat aatacgtatt tatatttaaa ataaaattat gt                     2144
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<210> 58
<211> 550
<212> PRT
<213> Ctenocephalides felis

<220>
<221> misc_feature
<222> (145)..(145)
<223> The 'Xaa' at location 145 stands for Asp, or Asn.

<400> 58

Met Ser Arg Val Ile Phe Leu Ser Cys Ile Phe Leu Phe Ser Phe Asn
1 5 10 15

Phe Ile Lys Cys Asp Ser Pro Thr Val Thr Leu Pro Gln Gly Glu Leu
20 25 30

Val Gly Lys Ala Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr
35 40 45

Thr Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys
50 55 60

Pro Pro Gln Lys Ala Glu Pro Trp Gln Gly Val Phe Asn Ala Thr Leu
65 70 75 80

Tyr Gly Asn Val Cys Lys Ser Leu Asn Phe Phe Leu Lys Lys Ile Glu
85 90 95

Gly Asp Glu Asp Cys Leu Val Val Asn Val Tyr Ala Pro Lys Thr Thr
100 105 110

Ser Asp Lys Lys Leu Pro Val Phe Phe Trp Val His Gly Gly Gly Phe
115 120 125

Val Thr Gly Ser Gly Asn Leu Glu Phe Gln Ser Pro Asp Tyr Leu Val
130 135 140

Xaa Phe Asp Val Ile Phe Val Thr Phe Asn Tyr Arg Leu Gly Pro Leu
145 150 155 160

Gly Phe Leu Asn Leu Glu Leu Glu Gly Ala Pro Gly Asn Val Gly Leu
165 170 175

Leu Asp Gln Val Ala Ala Leu Lys Trp Thr Lys Glu Asn Ile Glu Lys
180 185 190

Phe Gly Gly Asp Pro Glu Asn Ile Thr Ile Gly Gly Val Ser Ala Gly
195 200 205

Gly Ala Ser Val His Tyr Leu Leu Leu Ser His Thr Thr Thr Gly Leu
210 215 220

Tyr Lys Arg Ala Ile Ala Gln Ser Gly Ser Ala Phe Asn Pro Trp Ala
225 230 235 240

Phe Gln Arg His Pro Val Lys Arg Ser Leu Gln Leu Ala Glu Ile Leu
245 250 255

```
Gly His Pro Thr Asn Asn Thr Gln Asp Ala Leu Glu Phe Leu Gln Lys
           260                 265                 270

Ala Pro Val Asp Ser Leu Leu Lys Lys Met Pro Ala Glu Thr Glu Gly
       275                 280                 285

Glu Ile Ile Glu Glu Phe Val Phe Val Pro Ser Ile Glu Lys Val Phe
   290                 295                 300

Pro Ser His Gln Pro Phe Leu Glu Glu Ser Pro Leu Ala Arg Met Lys
305                 310                 315                 320

Ser Gly Ser Phe Asn Lys Val Pro Leu Leu Val Gly Phe Asn Ser Ala
                325                 330                 335

Glu Gly Leu Leu Phe Lys Phe Phe Met Lys Glu Lys Pro Glu Met Leu
           340                 345                 350

Asn Gln Ala Glu Ala Asp Phe Glu Arg Leu Val Pro Ala Glu Phe Glu
       355                 360                 365

Leu Val His Gly Ser Glu Glu Ser Lys Lys Leu Ala Glu Lys Ile Arg
   370                 375                 380

Lys Phe Tyr Phe Asp Asp Lys Pro Val Pro Glu Asn Glu Gln Lys Phe
385                 390                 395                 400

Ile Asp Leu Ile Gly Asp Ile Trp Phe Thr Arg Gly Val Asp Lys His
                405                 410                 415

Val Lys Leu Ser Val Glu Lys Gln Asp Glu Pro Val Tyr Tyr Tyr Glu
           420                 425                 430

Tyr Ser Phe Ser Glu Ser His Pro Ala Lys Gly Thr Phe Gly Asp His
       435                 440                 445

Asn Leu Thr Gly Ala Cys His Gly Glu Glu Leu Val Asn Leu Phe Lys
   450                 455                 460

Val Glu Met Met Lys Leu Glu Lys Asp Lys Pro Asn Val Leu Leu Thr
465                 470                 475                 480

Lys Asp Arg Val Leu Ala Met Trp Thr Asn Phe Ile Lys Asn Gly Asn
                485                 490                 495

Pro Thr Pro Glu Val Thr Glu Leu Leu Pro Val Lys Trp Glu Pro Ala
           500                 505                 510
```

Thr Lys Asp Lys Leu Asn Tyr Leu Asn Ile Asp Ala Thr Leu Thr Leu
515 520 525

Gly Thr Asn Pro Glu Ala Asn Arg Val Lys Phe Trp Glu Asp Ala Thr
530 535 540

Lys Ser Leu His Gly Gln
545 550

<210> 59
<211> 2144
<212> DNA
<213> Ctenocephalides felis

<400> 59
acataatttt attttaaata taaatacgta ttatcaaaat ataattttca ctaatgatat 60

cagaaatact aattatcaaa attattgaag agttaatttt atttttaagt taaacaaaaa 120

ttccgtttgg aattttactt tatttttggt attttcttta aaaaaaatta ttgaaaatat 180

cttatatttt tagttaatgt atttttactg attttagtgt atatataaaa atacttcaga 240

gtacttaata taacatatct attggaaatt ttgctaaaaa caaacgacgt tgtgttttga 300

aaattaaaac catgatattt caaaacaagc aaaacaagaa taaataaata aaattagaac 360

tgatacacat aagccaatac ataaaacata aaaattgtta ttttttaatt tttatttacc 420

taatatatta cctaaagtat ttaaaacaat tttcataaat tattattgac cgtgcaaaga 480

ttttgtggcg tcttcccaaa atttgactcg gtttgcctca ggatttgttc ccaaagttaa 540

ggtggcatca atgttcaaat aattcaactt gtcttttgtg gcaggttccc atttaactgg 600

caataattct gttacttcag gagtaggatt tccatttttg atgaagttag tccacatggc 660

aagtactcta tcttttgtta atagaacatt aggtttatct ttttccagct tcatcatctc 720

gactttgaat aaattcacaa gttcttctcc atggcatgca ccagtcagat tatgatcacc 780

aaatgttcct tttgcaggat gactttccga gaaggaatat tcataataat aaactggttc 840

gtcttgtttc tccacagaca acttgacatg cttgtcaaca cctctagtaa accaaatatc 900

tcctatcaag tcaataaatt tctgttcatt ttctggaacg ggtttatcgt caaagtaaaa 960

cttcctgatt ttttctgcaa gttttttcga ttcctctgat ccatggacta attcaaattc 1020

ggctggtacg agtctttcaa aatctgcttc agcttggttc agcatctctg gtttttcttt 1080

catgaagaat ttgaacaaaa gtccttctgc actgttaaat ccaactaata aaggtacttt 1140

gttaaaggat ccggatttca ttctggccaa tggtgattct tccaagaaag gttggtggga 1200

tgggaaaact ttttcaattg atggtacgaa gacaaactct tctattattt caccttctgt 1260

ttcagctggc attttcttca ggagactgtc tacgggggct ttttgtaaga attctaaagc 1320

atcttgagta ttgtttgtgg gatgacccaa tatctcagca agttgaagac tacgctttac 1380

tggatgtctt tggaaggccc atggattaaa agcacttcca ctttgagcaa ttgccctttt 1440

gtaaagtcca gtggttgtat gagataacaa aagataatga acacttgctc caccagcaga 1500

aacaccacca attgtaatat tttctggatc tccaccaaat ttctcaatgt tttctttggt 1560

ccatttcaga gctgccacct gatccaataa tcctacattt cctggagcac cctccaactc 1620

caaattcaga aatccgagag gtcccaatcg gtaattgaaa gttacgaaaa taacatcaaa 1680

atytactaaa taatctgggc tttggaattc taaatttccg gatccagtca caaaaccacc 1740

accatgaacc cagaaaaata ctggaagttt tttatcagaa gttgtttttg gtgcgtacac 1800

gtttactacc aagcagtctt cgtctccttc aattttcttc aagaagaaat ttaaagattt 1860

acacacattt ccgtataatg tggcgttgaa aacaccttgc catggctcag ctttctgtgg 1920

aggcttaaat ctaagttctc caacaggagg tttagcataa ggtacacctg tgtagctaaa 1980

atactctttt ccattttcgt tcgtcaaagc ttttccaacc aattcgcctt ggggcaaagt 2040

tacagtcggg gaatcacatt ttataaaatt aaaactaaac aaaaaaatac aacttaaaaa 2100

aataacacga gacatcttgg atctagacta ttgactatgt gtac 2144

<210> 60
<211> 1650
<212> DNA
<213> Ctenocephalides felis

<220>
<221> exon
<222> (1)..(1650)
<223>

<220>
<221> misc_feature
<222> (433)..(433)
<223> At nucleotide 433, r = a or g
At amino acid residue 145, Xaa = Asn or Asp

<400> 60

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atg tct cgt gtt att ttt tta agt tgt att ttt ttg ttt agt ttt aat       48
Met Ser Arg Val Ile Phe Leu Ser Cys Ile Phe Leu Phe Ser Phe Asn
1               5                   10                  15

ttt ata aaa tgt gat tcc ccg act gta act ttg ccc caa ggc gaa ttg       96
Phe Ile Lys Cys Asp Ser Pro Thr Val Thr Leu Pro Gln Gly Glu Leu
            20                  25                  30

gtt gga aaa gct ttg acg aac gaa aat gga aaa gag tat ttt agc tac      144
Val Gly Lys Ala Leu Thr Asn Glu Asn Gly Lys Glu Tyr Phe Ser Tyr
        35                  40                  45

aca ggt gta cct tat gct aaa cct cct gtt gga gaa ctt aga ttt aag      192
Thr Gly Val Pro Tyr Ala Lys Pro Pro Val Gly Glu Leu Arg Phe Lys
    50                  55                  60
```

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cct cca cag aaa gct gag cca tgg caa ggt gtt ttc aac gcc aca tta      240
Pro Pro Gln Lys Ala Glu Pro Trp Gln Gly Val Phe Asn Ala Thr Leu
65                  70                  75                  80

tac gga aat gtg tgt aaa tct tta aat ttc ttc ttg aag aaa att gaa      288
Tyr Gly Asn Val Cys Lys Ser Leu Asn Phe Phe Leu Lys Lys Ile Glu
                85                  90                  95

gga gac gaa gac tgc ttg gta gta aac gtg tac gca cca aaa aca act      336
Gly Asp Glu Asp Cys Leu Val Val Asn Val Tyr Ala Pro Lys Thr Thr
            100                 105                 110

tct gat aaa aaa ctt cca gta ttt ttc tgg gtt cat ggt ggt ggt ttt      384
Ser Asp Lys Lys Leu Pro Val Phe Phe Trp Val His Gly Gly Gly Phe
        115                 120                 125

gtg act gga tcc gga aat tta gaa ttc caa agc cca gat tat tta gta      432
Val Thr Gly Ser Gly Asn Leu Glu Phe Gln Ser Pro Asp Tyr Leu Val
    130                 135                 140

rat ttt gat gtt att ttc gta act ttc aat tac cga ttg gga cct ctc      480
Xaa Phe Asp Val Ile Phe Val Thr Phe Asn Tyr Arg Leu Gly Pro Leu
145                 150                 155                 160

gga ttt ctg aat ttg gag ttg gag ggt gct cca gga aat gta gga tta      528
Gly Phe Leu Asn Leu Glu Leu Glu Gly Ala Pro Gly Asn Val Gly Leu
                165                 170                 175

ttg gat cag gtg gca gct ctg aaa tgg acc aaa gaa aac att gag aaa      576
Leu Asp Gln Val Ala Ala Leu Lys Trp Thr Lys Glu Asn Ile Glu Lys
            180                 185                 190

ttt ggt gga gat cca gaa aat att aca att ggt ggt gtt tct gct ggt      624
Phe Gly Gly Asp Pro Glu Asn Ile Thr Ile Gly Gly Val Ser Ala Gly
        195                 200                 205

gga gca agt gtt cat tat ctt ttg tta tct cat aca acc act gga ctt      672
Gly Ala Ser Val His Tyr Leu Leu Leu Ser His Thr Thr Thr Gly Leu
    210                 215                 220

tac aaa agg gca att gct caa agt gga agt gct ttt aat cca tgg gcc      720
Tyr Lys Arg Ala Ile Ala Gln Ser Gly Ser Ala Phe Asn Pro Trp Ala
225                 230                 235                 240

ttc caa aga cat cca gta aag cgt agt ctt caa ctt gct gag ata ttg      768
Phe Gln Arg His Pro Val Lys Arg Ser Leu Gln Leu Ala Glu Ile Leu
                245                 250                 255

ggt cat ccc aca aac aat act caa gat gct tta gaa ttc tta caa aaa      816
Gly His Pro Thr Asn Asn Thr Gln Asp Ala Leu Glu Phe Leu Gln Lys
            260                 265                 270

gcc ccc gta gac agt ctc ctg aag aaa atg cca gct gaa aca gaa ggt      864
Ala Pro Val Asp Ser Leu Leu Lys Lys Met Pro Ala Glu Thr Glu Gly
        275                 280                 285

gaa ata ata gaa gag ttt gtc ttc gta cca tca att gaa aaa gtt ttc      912
Glu Ile Ile Glu Glu Phe Val Phe Val Pro Ser Ile Glu Lys Val Phe
    290                 295                 300

cca tcc cac caa cct ttc ttg gaa gaa tca cca ttg gcc aga atg aaa      960
Pro Ser His Gln Pro Phe Leu Glu Glu Ser Pro Leu Ala Arg Met Lys
305                 310                 315                 320
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tcc gga tcc ttt aac aaa gta cct tta tta gtt gga ttt aac agt gca      1008
Ser Gly Ser Phe Asn Lys Val Pro Leu Leu Val Gly Phe Asn Ser Ala
                325                 330                 335

gaa gga ctt ttg ttc aaa ttc ttc atg aaa gaa aaa cca gag atg ctg      1056
Glu Gly Leu Leu Phe Lys Phe Phe Met Lys Glu Lys Pro Glu Met Leu
            340                 345                 350

aac caa gct gaa gca gat ttt gaa aga ctc gta cca gcc gaa ttt gaa      1104
Asn Gln Ala Glu Ala Asp Phe Glu Arg Leu Val Pro Ala Glu Phe Glu
        355                 360                 365

tta gtc cat gga tca gag gaa tcg aaa aaa ctt gca gaa aaa atc agg      1152
Leu Val His Gly Ser Glu Glu Ser Lys Lys Leu Ala Glu Lys Ile Arg
    370                 375                 380

aag ttt tac ttt gac gat aaa ccc gtt cca gaa aat gaa cag aaa ttt      1200
Lys Phe Tyr Phe Asp Asp Lys Pro Val Pro Glu Asn Glu Gln Lys Phe
385                 390                 395                 400

att gac ttg ata gga gat att tgg ttt act aga ggt gtt gac aag cat      1248
Ile Asp Leu Ile Gly Asp Ile Trp Phe Thr Arg Gly Val Asp Lys His
                405                 410                 415

gtc aag ttg tct gtg gag aaa caa gac gaa cca gtt tat tat tat gaa      1296
Val Lys Leu Ser Val Glu Lys Gln Asp Glu Pro Val Tyr Tyr Tyr Glu
            420                 425                 430

tat tcc ttc tcg gaa agt cat cct gca aaa gga aca ttt ggt gat cat      1344
Tyr Ser Phe Ser Glu Ser His Pro Ala Lys Gly Thr Phe Gly Asp His
        435                 440                 445

aat ctg act ggt gca tgc cat gga gaa gaa ctt gtg aat tta ttc aaa      1392
Asn Leu Thr Gly Ala Cys His Gly Glu Glu Leu Val Asn Leu Phe Lys
    450                 455                 460

gtc gag atg atg aag ctg gaa aaa gat aaa cct aat gtt cta tta aca      1440
Val Glu Met Met Lys Leu Glu Lys Asp Lys Pro Asn Val Leu Leu Thr
465                 470                 475                 480

aaa gat aga gta ctt gcc atg tgg act aac ttc atc aaa aat gga aat      1488
Lys Asp Arg Val Leu Ala Met Trp Thr Asn Phe Ile Lys Asn Gly Asn
                485                 490                 495

cct act cct gaa gta aca gaa tta ttg cca gtt aaa tgg gaa cct gcc      1536
Pro Thr Pro Glu Val Thr Glu Leu Leu Pro Val Lys Trp Glu Pro Ala
            500                 505                 510

aca aaa gac aag ttg aat tat ttg aac att gat gcc acc tta act ttg      1584
Thr Lys Asp Lys Leu Asn Tyr Leu Asn Ile Asp Ala Thr Leu Thr Leu
        515                 520                 525

gga aca aat cct gag gca aac cga gtc aaa ttt tgg gaa gac gcc aca      1632
Gly Thr Asn Pro Glu Ala Asn Arg Val Lys Phe Trp Glu Asp Ala Thr
    530                 535                 540

aaa tct ttg cac ggt caa                                             1650
Lys Ser Leu His Gly Gln
545                 550
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<210> 61
<211> 1650
<212> DNA

<213> Ctenocephalides felis

<400> 61
ttgaccgtgc aaagattttg tggcgtcttc ccaaaatttg actcggtttg cctcaggatt 60

tgttcccaaa gttaaggtgg catcaatgtt caaataattc aacttgtctt ttgtggcagg 120

ttcccattta actggcaata attctgttac ttcaggagta ggatttccat ttttgatgaa 180

gttagtccac atggcaagta ctctatcttt tgttaataga acattaggtt tatcttttc 240

cagcttcatc atctcgactt tgaataaatt cacaagttct tctccatggc atgcaccagt 300

cagattatga tcaccaaatg ttccttttgc aggatgactt tccgagaagg aatattcata 360

ataataaact ggttcgtctt gtttctccac agacaacttg acatgcttgt caacacctct 420

agtaaaccaa atatctccta tcaagtcaat aaatttctgt tcattttctg gaacgggttt 480

atcgtcaaag taaaacttcc tgatttttc tgcaagtttt ttcgattcct ctgatccatg 540

gactaattca aattcggctg gtacgagtct ttcaaaatct gcttcagctt ggttcagcat 600

ctctggtttt tctttcatga agaatttgaa caaaagtcct tctgcactgt taaatccaac 660

taataaaggt actttgttaa aggatccgga tttcattctg gccaatggtg attcttccaa 720

gaaaggttgg tgggatggga aaacttttc aattgatggt acgaagacaa actcttctat 780

tatttcacct tctgtttcag ctggcatttt cttcaggaga ctgtctacgg gggctttttg 840

taagaattct aaagcatctt gagtattgtt tgtgggatga cccaatatct cagcaagttg 900

aagactacgc tttactggat gtctttggaa ggcccatgga ttaaaagcac ttccactttg 960

agcaattgcc cttttgtaaa gtccagtggt tgtatgagat aacaaaagat aatgaacact 1020

tgctccacca gcagaaacac caccaattgt aatattttct ggatctccac caaatttctc 1080

aatgttttct ttggtccatt tcagagctgc cacctgatcc aataatccta catttcctgg 1140

agcaccctcc aactccaaat tcagaaatcc gagaggtccc aatcggtaat tgaaagttac 1200

gaaaataaca tcaaaatyta ctaaataatc tgggctttgg aattctaaat ttccggatcc 1260

agtcacaaaa ccaccaccat gaacccagaa aaatactgga agtttttat cagaagttgt 1320

ttttggtgcg tacacgttta ctaccaagca gtcttcgtct ccttcaattt tcttcaagaa 1380

gaaatttaaa gatttacaca catttccgta taatgtggcg ttgaaaacac cttgccatgg 1440

ctcagctttc tgtggaggct taaatctaag ttctccaaca ggaggtttag cataaggtac 1500

acctgtgtag ctaaaatact cttttccatt ttcgttcgtc aaagcttttc caaccaattc 1560

gccttggggc aaagttacag tcggggaatc acattttata aaattaaaac taaacaaaaa 1620

aatacaactt aaaaaaataa cacgagacat 1650

<210> 62
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 62
aaactcgagt cccccgactg taactttgc 29

<210> 63
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 63
tcatctgcag ttattgactg tgcaaagttt ttgtgg 36

<210> 64
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 64
ttccggatcc ggctgatcta caagtgactt tg 32

<210> 65
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 65
tggtactcga gtcataaaaa tttattccaa aatc 34

<210> 66
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 66
aaaactgcag tataaatatg ttacctcaca gtgcattag 39

<210> 67
<211> 1987
<212> DNA
<213> Ctenocephalides felis

<220>
<221> CDS
<222> (231)..(1820)

<223>

<400> 67

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aattcacagt gtaaataatt ttatttgata taaatgtatt taatttttat tttaatctaa     60

ttttaattta aatatatata gttttattta taaaaaaata ttttttttat gatcgaaaag    120

aaatttttat ttatgtttat gagtgtgtgt tttggctatg atttacatta tttttgagct    180

agtataaaat taaaccatat tatattttgg atatataata acattttata atg tgt       236
                                                          Met Cys
                                                          1

gat cca tta cta aaa aca aca aca tat gga att ctg aaa ggc aag aaa       284
Asp Pro Leu Leu Lys Thr Thr Thr Tyr Gly Ile Leu Lys Gly Lys Lys
        5                  10                  15

gtt gta aac gaa aat ggt aaa att tac tat agt tac aca ggt ata ccc       332
Val Val Asn Glu Asn Gly Lys Ile Tyr Tyr Ser Tyr Thr Gly Ile Pro
    20                  25                  30

tat gca aaa tct cct gta aat gat ctc aga ttc aag cca cca caa aaa       380
Tyr Ala Lys Ser Pro Val Asn Asp Leu Arg Phe Lys Pro Pro Gln Lys
35                  40                  45                  50

ctt gat cct tgg aat ggt gtt ttt gac gcc act cag tat gga aat aat       428
Leu Asp Pro Trp Asn Gly Val Phe Asp Ala Thr Gln Tyr Gly Asn Asn
                55                  60                  65

tgt gct gct ggg aaa tgg ttt ttg aaa tca gct ggg ggt tgc gaa gat       476
Cys Ala Ala Gly Lys Trp Phe Leu Lys Ser Ala Gly Gly Cys Glu Asp
            70                  75                  80

tgc ctt tac tta aat atc tat gtc cca caa aac act tca gaa aat cct       524
Cys Leu Tyr Leu Asn Ile Tyr Val Pro Gln Asn Thr Ser Glu Asn Pro
        85                  90                  95

ttg cca gta atg ttt tgg att cat gga gga gca ttt gtg gtc gga tca       572
Leu Pro Val Met Phe Trp Ile His Gly Gly Ala Phe Val Val Gly Ser
    100                 105                 110

gga aat tct gat ata cat ggt cct gat tat tta ata gaa tat gat att       620
Gly Asn Ser Asp Ile His Gly Pro Asp Tyr Leu Ile Glu Tyr Asp Ile
115                 120                 125                 130

atc tta gta act att aat tat cgt cta gga cca ctt ggt ttt ctt aat       668
Ile Leu Val Thr Ile Asn Tyr Arg Leu Gly Pro Leu Gly Phe Leu Asn
                135                 140                 145

ttg gaa atc gaa gat gcg cct ggg aat gtt gga ttg atg gat caa gtt       716
Leu Glu Ile Glu Asp Ala Pro Gly Asn Val Gly Leu Met Asp Gln Val
            150                 155                 160

gca gcc cta aaa tgg gta aat gaa aat att gca acc ttt agt gga gac       764
Ala Ala Leu Lys Trp Val Asn Glu Asn Ile Ala Thr Phe Ser Gly Asp
        165                 170                 175

cca aaa aat att aca att tgt gga gca act gct gga gct gca agt gta       812
Pro Lys Asn Ile Thr Ile Cys Gly Ala Thr Ala Gly Ala Ala Ser Val
    180                 185                 190

cat tat cac att ttg tca caa ctt acc aaa ggt tta ttc cac aag gct       860
His Tyr His Ile Leu Ser Gln Leu Thr Lys Gly Leu Phe His Lys Ala
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195                 200                 205                 210

ata gca caa agt gga agt gct ttt aat ccc tgg gct ttc caa aaa aat      908
Ile Ala Gln Ser Gly Ser Ala Phe Asn Pro Trp Ala Phe Gln Lys Asn
                215                 220                 225

cct gtt aag aat gca ctt cga cta tgc aaa acc tta ggc ctt acc aca      956
Pro Val Lys Asn Ala Leu Arg Leu Cys Lys Thr Leu Gly Leu Thr Thr
            230                 235                 240

aac aac ctt caa gaa gcc ttg gat ttt ttg aaa aac cta cca gta gaa     1004
Asn Asn Leu Gln Glu Ala Leu Asp Phe Leu Lys Asn Leu Pro Val Glu
        245                 250                 255

aca ttg tta aat acc aaa tta ccc caa gaa att gat ggt caa ctg ctg     1052
Thr Leu Leu Asn Thr Lys Leu Pro Gln Glu Ile Asp Gly Gln Leu Leu
    260                 265                 270

gat gac ttc gtg ttt gta cct tcg att gaa aaa aca ttt cca gaa caa     1100
Asp Asp Phe Val Phe Val Pro Ser Ile Glu Lys Thr Phe Pro Glu Gln
275                 280                 285                 290

gat tcg tac tta act gac ttg cca ata cca ata ata aat tca gga aaa     1148
Asp Ser Tyr Leu Thr Asp Leu Pro Ile Pro Ile Ile Asn Ser Gly Lys
                295                 300                 305

ttc cac aaa gtt cca ttg ttg aca ggt tac aac agt gcc gaa ggc aat     1196
Phe His Lys Val Pro Leu Leu Thr Gly Tyr Asn Ser Ala Glu Gly Asn
            310                 315                 320

cta ttt ttc atg tac tta aaa aca gat cca gat tta tta aat aaa ttt     1244
Leu Phe Phe Met Tyr Leu Lys Thr Asp Pro Asp Leu Leu Asn Lys Phe
        325                 330                 335

gaa gct gat ttt gaa aga ttt ata cca act gac tta gaa tta cct ttg     1292
Glu Ala Asp Phe Glu Arg Phe Ile Pro Thr Asp Leu Glu Leu Pro Leu
    340                 345                 350

cga tca caa aaa tct att gca ctg ggt gaa gca atc agg gaa ttt tat     1340
Arg Ser Gln Lys Ser Ile Ala Leu Gly Glu Ala Ile Arg Glu Phe Tyr
355                 360                 365                 370

ttc caa aac aaa acc ata tca gaa aat atg cag aat ttt gta gat gtt     1388
Phe Gln Asn Lys Thr Ile Ser Glu Asn Met Gln Asn Phe Val Asp Val
                375                 380                 385

tta agt gat aat tgg ttt aca cgt gga att gat gag caa gta aag tta     1436
Leu Ser Asp Asn Trp Phe Thr Arg Gly Ile Asp Glu Gln Val Lys Leu
            390                 395                 400

act gtt aaa aat cag gaa gaa cca gtt ttt tat tat gtt tat aat ttt     1484
Thr Val Lys Asn Gln Glu Glu Pro Val Phe Tyr Tyr Val Tyr Asn Phe
        405                 410                 415

gat gaa aat tct cca agt cgg aaa gtt ttt ggt gat ttt gga ata aaa     1532
Asp Glu Asn Ser Pro Ser Arg Lys Val Phe Gly Asp Phe Gly Ile Lys
    420                 425                 430

ggc ggt ggt cat gct gat gaa ttg ggt aat ata ttt aaa gcc aaa agt     1580
Gly Gly Gly His Ala Asp Glu Leu Gly Asn Ile Phe Lys Ala Lys Ser
435                 440                 445                 450

gca aat ttt ggg aag gaa aca cca aat gct gtg ttg gtt cag aga agg     1628
Ala Asn Phe Gly Lys Glu Thr Pro Asn Ala Val Leu Val Gln Arg Arg
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                455                 460                 465

atg ctg gag atg tgg act aat ttt gct aaa ttt gga aat cct act cca     1676
Met Leu Glu Met Trp Thr Asn Phe Ala Lys Phe Gly Asn Pro Thr Pro
            470                 475                 480

gct att acg gat aca ctt cca ata aaa tgg gaa cct gct ttt aaa gaa     1724
Ala Ile Thr Asp Thr Leu Pro Ile Lys Trp Glu Pro Ala Phe Lys Glu
        485                 490                 495

aat atg act ttt gtt caa att gac att gat tta aat ttg agt act gat     1772
Asn Met Thr Phe Val Gln Ile Asp Ile Asp Leu Asn Leu Ser Thr Asp
    500                 505                 510

cca cta aaa agt cgt atg gaa ttt ggg aat aaa ata aaa tta tta aaa     1820
Pro Leu Lys Ser Arg Met Glu Phe Gly Asn Lys Ile Lys Leu Leu Lys
515                 520                 525                 530

taagtaacta tacttagcta aaccataata taccaaataa tagtatagga atacttcaca   1880

atttttttgtt acttcgttaa gtaaatttaa ttttttataa aaccaacttt tacgaataaa   1940

aaatgtaatt attttggaaa aaaaaaagaa aaaaaaaaaa aaaaaac                 1987
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<210> 68
<211> 530
<212> PRT
<213> Ctenocephalides felis

<400> 68

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Met Cys Asp Pro Leu Leu Lys Thr Thr Thr Tyr Gly Ile Leu Lys Gly
1               5                   10                  15

Lys Lys Val Val Asn Glu Asn Gly Lys Ile Tyr Tyr Ser Tyr Thr Gly
            20                  25                  30

Ile Pro Tyr Ala Lys Ser Pro Val Asn Asp Leu Arg Phe Lys Pro Pro
        35                  40                  45

Gln Lys Leu Asp Pro Trp Asn Gly Val Phe Asp Ala Thr Gln Tyr Gly
    50                  55                  60

Asn Asn Cys Ala Ala Gly Lys Trp Phe Leu Lys Ser Ala Gly Gly Cys
65                  70                  75                  80

Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro Gln Asn Thr Ser Glu
                85                  90                  95

Asn Pro Leu Pro Val Met Phe Trp Ile His Gly Gly Ala Phe Val Val
            100                 105                 110

Gly Ser Gly Asn Ser Asp Ile His Gly Pro Asp Tyr Leu Ile Glu Tyr
        115                 120                 125
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Asp Ile Ile Leu Val Thr Ile Asn Tyr Arg Leu Gly Pro Leu Gly Phe
    130                 135                 140

Leu Asn Leu Glu Ile Glu Asp Ala Pro Gly Asn Val Gly Leu Met Asp
145                 150                 155                 160

Gln Val Ala Ala Leu Lys Trp Val Asn Glu Asn Ile Ala Thr Phe Ser
                165                 170                 175

Gly Asp Pro Lys Asn Ile Thr Ile Cys Gly Ala Thr Ala Gly Ala Ala
            180                 185                 190

Ser Val His Tyr His Ile Leu Ser Gln Leu Thr Lys Gly Leu Phe His
        195                 200                 205

Lys Ala Ile Ala Gln Ser Gly Ser Ala Phe Asn Pro Trp Ala Phe Gln
    210                 215                 220

Lys Asn Pro Val Lys Asn Ala Leu Arg Leu Cys Lys Thr Leu Gly Leu
225                 230                 235                 240

Thr Thr Asn Asn Leu Gln Glu Ala Leu Asp Phe Leu Lys Asn Leu Pro
                245                 250                 255

Val Glu Thr Leu Leu Asn Thr Lys Leu Pro Gln Glu Ile Asp Gly Gln
            260                 265                 270

Leu Leu Asp Asp Phe Val Phe Val Pro Ser Ile Glu Lys Thr Phe Pro
        275                 280                 285

Glu Gln Asp Ser Tyr Leu Thr Asp Leu Pro Ile Pro Ile Ile Asn Ser
    290                 295                 300

Gly Lys Phe His Lys Val Pro Leu Leu Thr Gly Tyr Asn Ser Ala Glu
305                 310                 315                 320

Gly Asn Leu Phe Phe Met Tyr Leu Lys Thr Asp Pro Asp Leu Leu Asn
                325                 330                 335

Lys Phe Glu Ala Asp Phe Glu Arg Phe Ile Pro Thr Asp Leu Glu Leu
            340                 345                 350

Pro Leu Arg Ser Gln Lys Ser Ile Ala Leu Gly Glu Ala Ile Arg Glu
        355                 360                 365

Phe Tyr Phe Gln Asn Lys Thr Ile Ser Glu Asn Met Gln Asn Phe Val
    370                 375                 380
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Asp Val Leu Ser Asp Asn Trp Phe Thr Arg Gly Ile Asp Glu Gln Val
385                 390                 395                 400

Lys Leu Thr Val Lys Asn Gln Glu Glu Pro Val Phe Tyr Tyr Val Tyr
                405                 410                 415

Asn Phe Asp Glu Asn Ser Pro Ser Arg Lys Val Phe Gly Asp Phe Gly
            420                 425                 430

Ile Lys Gly Gly Gly His Ala Asp Glu Leu Gly Asn Ile Phe Lys Ala
        435                 440                 445

Lys Ser Ala Asn Phe Gly Lys Glu Thr Pro Asn Ala Val Leu Val Gln
    450                 455                 460

Arg Arg Met Leu Glu Met Trp Thr Asn Phe Ala Lys Phe Gly Asn Pro
465                 470                 475                 480

Thr Pro Ala Ile Thr Asp Thr Leu Pro Ile Lys Trp Glu Pro Ala Phe
                485                 490                 495

Lys Glu Asn Met Thr Phe Val Gln Ile Asp Ile Asp Leu Asn Leu Ser
            500                 505                 510

Thr Asp Pro Leu Lys Ser Arg Met Glu Phe Gly Asn Lys Ile Lys Leu
        515                 520                 525

Leu Lys
    530
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<210> 69
<211> 1987
<212> DNA
<213> Ctenocephalides felis

<400> 69

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gttggtttta taaaaaatta aatttactta acgaagtaac aaaaaattgt gaagtattcc    120

tatactatta tttggtatat tatggtttag ctaagtatag ttacttattt taataatttt    180

attttattcc caaattccat acgacttttt agtggatcag tactcaaatt taaatcaatg    240

tcaatttgaa caaaagtcat attttcttta aaagcaggtt cccattttat tggaagtgta    300

tccgtaatag ctggagtagg atttccaaat ttagcaaaat tagtccacat ctccagcatc    360

cttctctgaa ccaacacagc atttggtgtt tccttcccaa aatttgcact tttggcttta    420

aatatattac ccaattcatc agcatgacca ccgcctttta ttccaaaatc accaaaaact    480

ttccgacttg gagaattttc atcaaaatta taaacataat aaaaaactgg ttcttcctga    540
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ttttaacag ttaactttac ttgctcatca attccacgtg taaaccaatt atcacttaaa 600

acatctacaa aattctgcat attttctgat atggttttgt tttggaaata aaattccctg 660

attgcttcac ccagtgcaat agatttttgt gatcgcaaag gtaattctaa gtcagttggt 720

ataaatcttt caaaatcagc ttcaaattta tttaataaat ctggatctgt ttttaagtac 780

atgaaaaata gattgccttc ggcactgttg taacctgtca acaatggaac tttgtggaat 840

tttcctgaat ttattattgg tattggcaag tcagttaagt acgaatcttg ttctggaaat 900

gttttttcaa tcgaaggtac aaacacgaag tcatccagca gttgaccatc aatttcttgg 960

ggtaatttgg tatttaacaa tgtttctact ggtaggtttt tcaaaaaatc caaggcttct 1020

tgaaggttgt ttgtggtaag gcctaaggtt ttgcatagtc gaagtgcatt cttaacagga 1080

ttttttgga aagcccaggg attaaaagca cttccacttt gtgctatagc cttgtggaat 1140

aaacctttgg taagttgtga caaaatgtga taatgtacac ttgcagctcc agcagttgct 1200

ccacaaattg taatattttt tgggtctcca ctaaaggttg caatattttc atttacccat 1260

tttagggctg caacttgatc catcaatcca acattcccag gcgcatcttc gatttccaaa 1320

ttaagaaaac caagtggtcc tagacgataa ttaatagtta ctaagataat atcatattct 1380

attaaataat caggaccatg tatatcagaa tttcctgatc cgaccacaaa tgctcctcca 1440

tgaatccaaa acattactgg caaaggattt tctgaagtgt tttgtgggac atagatattt 1500

aagtaaaggc aatcttcgca acccccagct gatttcaaaa accatttccc agcagcacaa 1560

ttatttccat actgagtggc gtcaaaaaca ccattccaag gatcaagttt ttgtggtggc 1620

ttgaatctga gatcatttac aggagatttt gcatagggta tacctgtgta actatagtaa 1680

attttaccat tttcgtttac aactttcttg cctttcagaa ttccatatgt tgttgttttt 1740

agtaatggat cacacattat aaaatgttat tatatatcca aaatataata tggtttaatt 1800

ttatactagc tcaaaaataa tgtaaatcat agccaaaaca cacactcata aacataaata 1860

aaaatttctt ttcgatcata aaaaaaatat ttttttataa ataaaactat atatatttaa 1920

attaaaatta gattaaaata aaaattaaat acatttatat caaataaaat tatttacact 1980

gtgaatt 1987

<210> 70
<211> 1590
<212> DNA
<213> Ctenocephalides felis

<220>
<221> exon
<222> (1)..(1590)
<223>

<400> 70
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Met Cys Asp Pro Leu Leu Lys Thr Thr Thr Tyr Gly Ile Leu Lys Gly
1               5                  10                  15

aag aaa gtt gta aac gaa aat ggt aaa att tac tat agt tac aca ggt      96
Lys Lys Val Val Asn Glu Asn Gly Lys Ile Tyr Tyr Ser Tyr Thr Gly
            20                  25                  30

ata ccc tat gca aaa tct cct gta aat gat ctc aga ttc aag cca cca     144
Ile Pro Tyr Ala Lys Ser Pro Val Asn Asp Leu Arg Phe Lys Pro Pro
        35                  40                  45

caa aaa ctt gat cct tgg aat ggt gtt ttt gac gcc act cag tat gga     192
Gln Lys Leu Asp Pro Trp Asn Gly Val Phe Asp Ala Thr Gln Tyr Gly
    50                  55                  60

aat aat tgt gct gct ggg aaa tgg ttt ttg aaa tca gct ggg ggt tgc     240
Asn Asn Cys Ala Ala Gly Lys Trp Phe Leu Lys Ser Ala Gly Gly Cys
65                  70                  75                  80

gaa gat tgc ctt tac tta aat atc tat gtc cca caa aac act tca gaa     288
Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro Gln Asn Thr Ser Glu
                85                  90                  95

aat cct ttg cca gta atg ttt tgg att cat gga gga gca ttt gtg gtc     336
Asn Pro Leu Pro Val Met Phe Trp Ile His Gly Gly Ala Phe Val Val
            100                 105                 110

gga tca gga aat tct gat ata cat ggt cct gat tat tta ata gaa tat     384
Gly Ser Gly Asn Ser Asp Ile His Gly Pro Asp Tyr Leu Ile Glu Tyr
        115                 120                 125

gat att atc tta gta act att aat tat cgt cta gga cca ctt ggt ttt     432
Asp Ile Ile Leu Val Thr Ile Asn Tyr Arg Leu Gly Pro Leu Gly Phe
    130                 135                 140

ctt aat ttg gaa atc gaa gat gcg cct ggg aat gtt gga ttg atg gat     480
Leu Asn Leu Glu Ile Glu Asp Ala Pro Gly Asn Val Gly Leu Met Asp
145                 150                 155                 160

caa gtt gca gcc cta aaa tgg gta aat gaa aat att gca acc ttt agt     528
Gln Val Ala Ala Leu Lys Trp Val Asn Glu Asn Ile Ala Thr Phe Ser
                165                 170                 175

gga gac cca aaa aat att aca att tgt gga gca act gct gga gct gca     576
Gly Asp Pro Lys Asn Ile Thr Ile Cys Gly Ala Thr Ala Gly Ala Ala
            180                 185                 190

agt gta cat tat cac att ttg tca caa ctt acc aaa ggt tta ttc cac     624
Ser Val His Tyr His Ile Leu Ser Gln Leu Thr Lys Gly Leu Phe His
        195                 200                 205

aag gct ata gca caa agt gga agt gct ttt aat ccc tgg gct ttc caa     672
Lys Ala Ile Ala Gln Ser Gly Ser Ala Phe Asn Pro Trp Ala Phe Gln
    210                 215                 220

aaa aat cct gtt aag aat gca ctt cga cta tgc aaa acc tta ggc ctt     720
Lys Asn Pro Val Lys Asn Ala Leu Arg Leu Cys Lys Thr Leu Gly Leu
225                 230                 235                 240

acc aca aac aac ctt caa gaa gcc ttg gat ttt ttg aaa aac cta cca     768
Thr Thr Asn Asn Leu Gln Glu Ala Leu Asp Phe Leu Lys Asn Leu Pro
                245                 250                 255

gta gaa aca ttg tta aat acc aaa tta ccc caa gaa att gat ggt caa     816
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Val Glu Thr Leu Leu Asn Thr Lys Leu Pro Gln Glu Ile Asp Gly Gln
            260                 265                 270

ctg ctg gat gac ttc gtg ttt gta cct tcg att gaa aaa aca ttt cca      864
Leu Leu Asp Asp Phe Val Phe Val Pro Ser Ile Glu Lys Thr Phe Pro
        275                 280                 285

gaa caa gat tcg tac tta act gac ttg cca ata cca ata ata aat tca      912
Glu Gln Asp Ser Tyr Leu Thr Asp Leu Pro Ile Pro Ile Ile Asn Ser
    290                 295                 300

gga aaa ttc cac aaa gtt cca ttg ttg aca ggt tac aac agt gcc gaa      960
Gly Lys Phe His Lys Val Pro Leu Leu Thr Gly Tyr Asn Ser Ala Glu
305                 310                 315                 320

ggc aat cta ttt ttc atg tac tta aaa aca gat cca gat tta tta aat     1008
Gly Asn Leu Phe Phe Met Tyr Leu Lys Thr Asp Pro Asp Leu Leu Asn
                325                 330                 335

aaa ttt gaa gct gat ttt gaa aga ttt ata cca act gac tta gaa tta     1056
Lys Phe Glu Ala Asp Phe Glu Arg Phe Ile Pro Thr Asp Leu Glu Leu
            340                 345                 350

cct ttg cga tca caa aaa tct att gca ctg ggt gaa gca atc agg gaa     1104
Pro Leu Arg Ser Gln Lys Ser Ile Ala Leu Gly Glu Ala Ile Arg Glu
        355                 360                 365

ttt tat ttc caa aac aaa acc ata tca gaa aat atg cag aat ttt gta     1152
Phe Tyr Phe Gln Asn Lys Thr Ile Ser Glu Asn Met Gln Asn Phe Val
    370                 375                 380

gat gtt tta agt gat aat tgg ttt aca cgt gga att gat gag caa gta     1200
Asp Val Leu Ser Asp Asn Trp Phe Thr Arg Gly Ile Asp Glu Gln Val
385                 390                 395                 400

aag tta act gtt aaa aat cag gaa gaa cca gtt ttt tat tat gtt tat     1248
Lys Leu Thr Val Lys Asn Gln Glu Glu Pro Val Phe Tyr Tyr Val Tyr
                405                 410                 415

aat ttt gat gaa aat tct cca agt cgg aaa gtt ttt ggt gat ttt gga     1296
Asn Phe Asp Glu Asn Ser Pro Ser Arg Lys Val Phe Gly Asp Phe Gly
            420                 425                 430

ata aaa ggc ggt ggt cat gct gat gaa ttg ggt aat ata ttt aaa gcc     1344
Ile Lys Gly Gly Gly His Ala Asp Glu Leu Gly Asn Ile Phe Lys Ala
        435                 440                 445

aaa agt gca aat ttt ggg aag gaa aca cca aat gct gtg ttg gtt cag     1392
Lys Ser Ala Asn Phe Gly Lys Glu Thr Pro Asn Ala Val Leu Val Gln
    450                 455                 460

aga agg atg ctg gag atg tgg act aat ttt gct aaa ttt gga aat cct     1440
Arg Arg Met Leu Glu Met Trp Thr Asn Phe Ala Lys Phe Gly Asn Pro
465                 470                 475                 480

act cca gct att acg gat aca ctt cca ata aaa tgg gaa cct gct ttt     1488
Thr Pro Ala Ile Thr Asp Thr Leu Pro Ile Lys Trp Glu Pro Ala Phe
                485                 490                 495

aaa gaa aat atg act ttt gtt caa att gac att gat tta aat ttg agt     1536
Lys Glu Asn Met Thr Phe Val Gln Ile Asp Ile Asp Leu Asn Leu Ser
            500                 505                 510

act gat cca cta aaa agt cgt atg gaa ttt ggg aat aaa ata aaa tta     1584
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Thr Asp Pro Leu Lys Ser Arg Met Glu Phe Gly Asn Lys Ile Lys Leu
515 520 525

tta aaa 1590
Leu Lys
530

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<212> DNA
<213> Ctenocephalides felis

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atttaaatca atgtcaattt gaacaaaagt catattttct ttaaaagcag gttcccattt 120

tattggaagt gtatccgtaa tagctggagt aggatttcca aatttagcaa aattagtcca 180

catctccagc atccttctct gaaccaacac agcatttggt gtttccttcc caaaatttgc 240

acttttggct ttaaatatat tacccaattc atcagcatga ccaccgcctt ttattccaaa 300

atcaccaaaa actttccgac ttggagaatt ttcatcaaaa ttataaacat aataaaaaac 360

tggttcttcc tgatttttaa cagttaactt tacttgctca tcaattccac gtgtaaacca 420

attatcactt aaaacatcta caaaattctg catattttct gatatggttt tgttttggaa 480

ataaaattcc ctgattgctt cacccagtgc aatagatttt tgtgatcgca aaggtaattc 540

taagtcagtt ggtataaatc tttcaaaatc agcttcaaat ttatttaata aatctggatc 600

tgtttttaag tacatgaaaa atagattgcc ttcggcactg ttgtaacctg tcaacaatgg 660

aactttgtgg aattttcctg aatttattat tggtattggc aagtcagtta agtacgaatc 720

ttgttctgga aatgtttttt caatcgaagg tacaaacacg aagtcatcca gcagttgacc 780

atcaatttct tggggtaatt tggtatttaa caatgtttct actggtaggt ttttcaaaaa 840

atccaaggct tcttgaaggt tgtttgtggt aaggcctaag gttttgcata gtcgaagtgc 900

attcttaaca ggatttttt ggaaagccca gggattaaaa gcacttccac tttgtgctat 960

agccttgtgg aataaacctt tggtaagttg tgacaaaatg tgataatgta cacttgcagc 1020

tccagcagtt gctccacaaa ttgtaatatt ttttgggtct ccactaaagg ttgcaatatt 1080

ttcatttacc cattttaggg ctgcaacttg atccatcaat ccaacattcc caggcgcatc 1140

ttcgatttcc aaattaagaa aaccaagtgg tcctagacga taattaatag ttactaagat 1200

aatatcatat tctattaaat aatcaggacc atgtatatca gaatttcctg atccgaccac 1260

aaatgctcct ccatgaatcc aaaacattac tggcaaagga ttttctgaag tgttttgtgg 1320

gacatagata tttaagtaaa ggcaatcttc gcaaccccca gctgatttca aaaaccattt 1380

cccagcagca caattatttc catactgagt ggcgtcaaaa acaccattcc aaggatcaag 1440

tttttgtggt ggcttgaatc tgagatcatt tacaggagat tttgcatagg gtatacctgt 1500

gtaactatag taaattttac cattttcgtt tacaactttc ttgcctttca gaattccata 1560

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   1               5                  10                  15

ttt gga cct gat tat ttg atc agg gaa gga att att ttg gtc act atc       95
Phe Gly Pro Asp Tyr Leu Ile Arg Glu Gly Ile Ile Leu Val Thr Ile
                20                  25                  30

aac tat aga tta gga gtt ttc ggt ttt cta tca gcg ccg gaa tgg gat      143
Asn Tyr Arg Leu Gly Val Phe Gly Phe Leu Ser Ala Pro Glu Trp Asp
            35                  40                  45

atc cat gga aat atg ggt cta aaa gac cag aga ttg gca cta aaa tgg      191
Ile His Gly Asn Met Gly Leu Lys Asp Gln Arg Leu Ala Leu Lys Trp
        50                  55                  60

gtt tac gac aac atc gaa aag ttt ggt gga gac aga gaa aaa att aca      239
Val Tyr Asp Asn Ile Glu Lys Phe Gly Gly Asp Arg Glu Lys Ile Thr
    65                  70                  75

att gct gga gaa tct gct gga gca gca agt gtc cat ttt ctg atg atg      287
Ile Ala Gly Glu Ser Ala Gly Ala Ala Ser Val His Phe Leu Met Met
80                  85                  90                  95

gac aac tcg act aga aaa tac tac caa agg gcc att ttg cag agt ggg      335
Asp Asn Ser Thr Arg Lys Tyr Tyr Gln Arg Ala Ile Leu Gln Ser Gly
                100                 105                 110

aca tta cta aat ccg act gct aat caa att caa ctt ctg cat aga ttt      383
Thr Leu Leu Asn Pro Thr Ala Asn Gln Ile Gln Leu Leu His Arg Phe
            115                 120                 125

gaa aaa ctc aaa caa gtg cta aac atc acg caa aaa caa gaa ctc cta      431
Glu Lys Leu Lys Gln Val Leu Asn Ile Thr Gln Lys Gln Glu Leu Leu
        130                 135                 140

aac ctg gat aaa aac cta att tta cga gca gcc tta aac aga gtt cct      479
Asn Leu Asp Lys Asn Leu Ile Leu Arg Ala Ala Leu Asn Arg Val Pro
    145                 150                 155

gat agc aac gac cat gac cga gac aca gta cca gta ttt aat cca gtc      527
Asp Ser Asn Asp His Asp Arg Asp Thr Val Pro Val Phe Asn Pro Val
160                 165                 170                 175

tta gaa tca cca gaa tct cca gat cca ata aca ttt cca tct gcc ttg      575
Leu Glu Ser Pro Glu Ser Pro Asp Pro Ile Thr Phe Pro Ser Ala Leu
                180                 185                 190
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gaa aga atg aga aat ggt gaa ttt cct gat gtc gat gtc atc att ggt      623
Glu Arg Met Arg Asn Gly Glu Phe Pro Asp Val Asp Val Ile Ile Gly
            195                 200                 205

ttc aat agt gct gaa ggt tta aga tct                                  650
Phe Asn Ser Ala Glu Gly Leu Arg Ser
        210                 215


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<211>  216
<212>  PRT
<213>  Ctenocephalides felis

<400>  73

Ile His Gly Gly Ala Phe Asn Gln Gly Ser Gly Ser Tyr Asn Phe Phe
1               5                   10                  15

Gly Pro Asp Tyr Leu Ile Arg Glu Gly Ile Ile Leu Val Thr Ile Asn
            20                  25                  30

Tyr Arg Leu Gly Val Phe Gly Phe Leu Ser Ala Pro Glu Trp Asp Ile
        35                  40                  45

His Gly Asn Met Gly Leu Lys Asp Gln Arg Leu Ala Leu Lys Trp Val
    50                  55                  60

Tyr Asp Asn Ile Glu Lys Phe Gly Gly Asp Arg Glu Lys Ile Thr Ile
65                  70                  75                  80

Ala Gly Glu Ser Ala Gly Ala Ala Ser Val His Phe Leu Met Met Asp
                85                  90                  95

Asn Ser Thr Arg Lys Tyr Tyr Gln Arg Ala Ile Leu Gln Ser Gly Thr
            100                 105                 110

Leu Leu Asn Pro Thr Ala Asn Gln Ile Gln Leu Leu His Arg Phe Glu
        115                 120                 125

Lys Leu Lys Gln Val Leu Asn Ile Thr Gln Lys Gln Glu Leu Leu Asn
    130                 135                 140

Leu Asp Lys Asn Leu Ile Leu Arg Ala Ala Leu Asn Arg Val Pro Asp
145                 150                 155                 160

Ser Asn Asp His Asp Arg Asp Thr Val Pro Val Phe Asn Pro Val Leu
                165                 170                 175

Glu Ser Pro Glu Ser Pro Asp Pro Ile Thr Phe Pro Ser Ala Leu Glu
            180                 185                 190
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Arg Met Arg Asn Gly Glu Phe Pro Asp Val Asp Val Ile Ile Gly Phe
        195                 200                 205

Asn Ser Ala Glu Gly Leu Arg Ser
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<400>  74

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1               5                   10                  15

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<210>  76
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   Gln Gly Glu Leu Val Gly Lys Ala Leu Thr Asn Glu Asn Gly Lys
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   1               5                  10                  15

gag tat ttt agc tac aca ggt gtg cct tat gct aaa cct cca gtt gga       95
Glu Tyr Phe Ser Tyr Thr Gly Val Pro Tyr Ala Lys Pro Pro Val Gly
                20                  25                  30

gaa ctt aga ttt aag cct cca cag aaa gct gag cca tgg aat ggt gtt      143
Glu Leu Arg Phe Lys Pro Pro Gln Lys Ala Glu Pro Trp Asn Gly Val
            35                  40                  45

ttc aac gcc aca tca cat gga aat gtg tgc aaa gct ttg aat ttc ttc      191
Phe Asn Ala Thr Ser His Gly Asn Val Cys Lys Ala Leu Asn Phe Phe
        50                  55                  60

ttg aaa aaa att gaa gga gac gaa gac tgc ttg ttg gtg aat gtg tac      239
Leu Lys Lys Ile Glu Gly Asp Glu Asp Cys Leu Leu Val Asn Val Tyr
    65                  70                  75

gca cca aaa aca act tct gac aaa aaa ctt cca gta ttt ttc tgg gtt      287
Ala Pro Lys Thr Thr Ser Asp Lys Lys Leu Pro Val Phe Phe Trp Val
80                  85                  90                  95

cat ggt ggc ggt ttt gtg act gga tcc gga aat tta gaa ttt caa agc      335
His Gly Gly Gly Phe Val Thr Gly Ser Gly Asn Leu Glu Phe Gln Ser
                100                 105                 110

cca gat tat tta gta aat tat gat gtt att ttt gta act ttc aat tac      383
Pro Asp Tyr Leu Val Asn Tyr Asp Val Ile Phe Val Thr Phe Asn Tyr
            115                 120                 125

cga ttg gga cca ctc gga ttt ttg aat ttg gag ttg gaa ggt gct cct      431
Arg Leu Gly Pro Leu Gly Phe Leu Asn Leu Glu Leu Glu Gly Ala Pro
        130                 135                 140

gga aat gta gga tta ttg gat cag gta gca gct ttg aaa tgg acc aaa      479
Gly Asn Val Gly Leu Leu Asp Gln Val Ala Ala Leu Lys Trp Thr Lys
    145                 150                 155

gaa aat att gag aaa ttt ggt gga gat cca gaa aat att aca att ggt      527
Glu Asn Ile Glu Lys Phe Gly Gly Asp Pro Glu Asn Ile Thr Ile Gly
160                 165                 170                 175

ggt gtt tct gct ggt gga gca agt gtt cat tat ctt tta ttg tca cat      575
Gly Val Ser Ala Gly Gly Ala Ser Val His Tyr Leu Leu Leu Ser His
                180                 185                 190

aca acc act gga ctt tac aaa agg gca att gct caa agt gga agt gct      623
Thr Thr Thr Gly Leu Tyr Lys Arg Ala Ile Ala Gln Ser Gly Ser Ala
            195                 200                 205

tta aat cca tgg gcc ttc caa aga cat cca gta aag cgt agt ctt caa      671
Leu Asn Pro Trp Ala Phe Gln Arg His Pro Val Lys Arg Ser Leu Gln
        210                 215                 220

ctt gct gag ata tta ggt cat ccc aca aac aac act caa gat gct tta      719
Leu Ala Glu Ile Leu Gly His Pro Thr Asn Asn Thr Gln Asp Ala Leu
    225                 230                 235

gaa ttc tta caa aaa gcc cca gta gac agt ctc ctg aaa aaa atg cca      767
Glu Phe Leu Gln Lys Ala Pro Val Asp Ser Leu Leu Lys Lys Met Pro
240                 245                 250                 255

gct gaa aca gaa ggt gaa ata ata gaa gag ttc gtc ttc gta cca tca      815
Ala Glu Thr Glu Gly Glu Ile Ile Glu Glu Phe Val Phe Val Pro Ser
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                    260                 265                 270

att gaa aaa gtt ttc cca tcc cac caa cct ttc ttg gaa gaa tca cca      863
Ile Glu Lys Val Phe Pro Ser His Gln Pro Phe Leu Glu Glu Ser Pro
            275                 280                 285

ttg gcc aga atg aaa tct gga tcc ttt aac aaa gta cct tta tta gtt      911
Leu Ala Arg Met Lys Ser Gly Ser Phe Asn Lys Val Pro Leu Leu Val
        290                 295                 300

gga ttc aac agc gca gaa gga ctt ttg tac aaa ttc ttt atg aaa gaa      959
Gly Phe Asn Ser Ala Glu Gly Leu Leu Tyr Lys Phe Phe Met Lys Glu
    305                 310                 315

aaa cca gag atg ctg aac caa gct gaa gca gat ttc gaa aga ctc gta     1007
Lys Pro Glu Met Leu Asn Gln Ala Glu Ala Asp Phe Glu Arg Leu Val
320                 325                 330                 335

cca gcc gaa ttt gaa tta gcc cat gga tca gaa gaa tcg aaa aaa ctt     1055
Pro Ala Glu Phe Glu Leu Ala His Gly Ser Glu Glu Ser Lys Lys Leu
                340                 345                 350

gca gaa aaa atc agg aag ttt tac ttt gac gat aaa ccc gtt cct gaa     1103
Ala Glu Lys Ile Arg Lys Phe Tyr Phe Asp Asp Lys Pro Val Pro Glu
            355                 360                 365

aat gag cag aaa ttt att gac ttg ata gga gat att tgg ttt act aga     1151
Asn Glu Gln Lys Phe Ile Asp Leu Ile Gly Asp Ile Trp Phe Thr Arg
        370                 375                 380

ggc att gac aag cat gtc aag ttg tct gta gaa aaa caa gac gag cca     1199
Gly Ile Asp Lys His Val Lys Leu Ser Val Glu Lys Gln Asp Glu Pro
    385                 390                 395

gta tat tat tat gaa tat tct ttc tct gaa agt cat cct gca aaa gga     1247
Val Tyr Tyr Tyr Glu Tyr Ser Phe Ser Glu Ser His Pro Ala Lys Gly
400                 405                 410                 415

aca ttt ggt gac cat aac ttg act gga gca tgt cat ggt gaa gaa ctt     1295
Thr Phe Gly Asp His Asn Leu Thr Gly Ala Cys His Gly Glu Glu Leu
                420                 425                 430

gtg aat tta ttc aaa gtc gag atg atg aag ctg gaa aaa gat aaa ccg     1343
Val Asn Leu Phe Lys Val Glu Met Met Lys Leu Glu Lys Asp Lys Pro
            435                 440                 445

aat gtt tta tta aca aaa gat agg gta ctt gct atg tgg acg aac ttc     1391
Asn Val Leu Leu Thr Lys Asp Arg Val Leu Ala Met Trp Thr Asn Phe
        450                 455                 460

atc aaa aat gga aat cct act cct gaa gta act gaa tta ttg cca gtt     1439
Ile Lys Asn Gly Asn Pro Thr Pro Glu Val Thr Glu Leu Leu Pro Val
    465                 470                 475

aaa tgg gaa cct gcc aca aaa gac aag ttg aat tat ttg aac att gat g   1488
Lys Trp Glu Pro Ala Thr Lys Asp Lys Leu Asn Tyr Leu Asn Ile Asp
480                 485                 490                 495
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